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4	390.4	79.3	727	10	B1521608	B1521608 603081449
5	388.4	78.9	785	10	B1829728	B1829728 603079792
6	381	77.4	545	9	AW393182	AW393182 CM2-ST028
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15	328.4	66.7	501	10	B1822872	B1822872 603040310
16	313.8	63.8	538	9	AW393184	AW393184 CM2-ST028
17	310	63.0	463	10	BF375600	BF375600 CM2-ST028

18	291.6	59.3	613	10	B1961937	B1961937 MONOI_8_F
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22	270.6	55.0	1224	11	AK009721	AK009721 Mus muscu
23	270.6	55.0	1314	11	AK003370	AK003370 Mus muscu
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26	265.4	53.9	471	9	AM9393180	AM9393180 CM2-ST028
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28	260.4	52.9	661	9	AM9393187	AM9393187 CM2-ST028
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43	140.2	28.5	432	10	BE200242	BE200242 ug61h04_x
44	137.8	28.0	432	10	BF042057	BF042057 BP250023A
45	129	26.2	267	9	AM9393207	AM9393207 CM2-ST028

ALIGNMENTS

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS
AA311795	451 bp	MRNA	linear	EST 19-APR-1997			
EST192531	Jurkat T-cells VI Homo sapiens CDNA 5' end similar to similar to Hypothetical protein C9, mRNA sequence.						
AA311795							
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EST.							
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
1 (bases 1 to 451)							
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult							
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O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,							
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Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,							
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Dimke,D., Feng,D.-F., Fertle,A., Fischer,C., Hastings,G.A., He,W.W.							
, Hu,J.S., Hungen,J.M., Gruber,J., Hudson,P., Kim,A.R., Kozak,D.L.,							
Kunsch,C., Gungun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L.,							
Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon							
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and							
Verter,J.C.							
Initial assessment of human gene diversity and expression patterns							
based upon 83 million nucleotides of cDNA sequence							
Nature 377 (6547 Suppl), 3-174 (1995)							
96026280							
Other ESTs: TH023801							
Contact: Kerlavage, AR							
Bioinformatics							
The Institute for Genomic Research							
9712 Medical Center Drive, Rockville, MD 20850 USA							
Tel: 3018699056							

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M3 Reverse..

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 similar to Hypothetical protein C9, mRNA sequence.
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 1 (bases 1 to 451)
 Adams, M.D., Kervase, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
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 Mel, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon
 M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
 Venter, J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl.), 3-174 (1995)
 96026280
 Other_ESTs: THC123801
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlavet@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
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 63 ProAsnPheserIleLeuTyThrLeuGlnGlnGlySerPheIleGluH 79
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 741)
 NIH-MGC <http://mgc.ncl.nih.gov/>,
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 21:44:59 ; Search time 1604.11 Seconds
(Without alignments)
4139.680 Million cell updates/sec

Title: US-09-786-130-32

Perfect score: 492

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Scoring table: IDENTITY_NUC
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Searched: 13736207 seqs, 674847542 residues
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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: em_gss_liv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	447.4	90.9	451	AA311795	AA311795 EST192531
2	447.4	90.9	547	AW962849	AW962849 EST374922
3	395	80.3	741	B1824342	B1824342 603040762
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10	363.2	73.8	515	BF375685	BF375685 RC5-ST030
11	360.4	73.3	531	AW393201	AW393201 CM2-ST028
12	350.8	71.3	754	BG775971	BG775971 602650008
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24	270.6	55.0	1334	11	AK008452	AK008452 Mus muscu
25	269	54.7	386	10	BF724662	BF724662 B07409.Y
26	265.4	53.9	471	9	AW393180	AW393180 CM2-ST028
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30	250.4	50.9	685	10	BE381966	BE381966 601271915
31	246.8	50.2	458	9	AA980066	AA980066 ua28b09.x
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41	153	31.1	218	10	BF375598	BF375598 CM2-ST028
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44	137.8	28.0	432	10	BF042057	BF042057 BP250023A
45	129	26.2	267	9	AW393207	AW393207 CM2-ST028

ALIGNMENTS

RESULT 1
AA311795 451 bp mRNA linear EST 19-Apr-1997
EST182531 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to
LOCUS similar to Hypothetical protein C9, mRNA sequence.

ACCESSION AA311795 GI:1964144
VERSION AA311795.1 GI:1964144
KEYWORDS EST.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 451)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulton,R.A., Bult

AUTHORS

C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wei,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,
L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodak,A.,
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Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
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Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
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M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.

TITLE

Initial assessment of human gene diversity and expression patterns
Nature 377 (6547 Suppl.), 3-174 (1995)

JOURNAL

Medline 96026280
Contact: Kerlavage, AR

COMMENT

Other ESTs: TH0123801
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056

Fax: 3016699423
 Email: arterlavet@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES

SOURCE

Location/Qualifiers

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Query Match

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 VERSION EST.
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM human.
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 547)
 Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gasparid,R., Gay,C., Holt
 J.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
 Quackenbush,J.
 Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray

JOURNAL Unpublished (2000)
 COMMENT Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 180

FEATURES

SOURCE

Seq primer: Reverse.

Location/Qualifiers

1..547
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="MAGE resequences, MAGC"
 /note="Vector: pBluescriptSKm"

BASE COUNT 115 a 183 c 145 g 104 t
 ORIGIN

Query Match

Best Local Similarity 90.9%; Score 447.4; DB 9; Length 547;
 /Matches 451; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 36 ctccagttagaagacaaaggacccttgcctcccaagcccccagtggtcccaagcagctaa 95
 Db 1 CTCAAGTTAGAAACACAAAGAGACCCCTCCCTCCAGCCCCAGTGTCCAGCAGCTAA 60
 Oy 96 gcaagtgccagcagcaltggaagtgacgtgacagagtggaagtgcacatgaaatggaagc 155
 Db 61 GCAGTGTCCAGCAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGC 120
 Oy 156 gagcttactcctgtgtgtgcctgacgcgcttcccaactcaagcactctactgtgtg 215
 Db 121 GAGCTTATCCTGT 180
 Oy 216 caatgtgttccttcatgtgacacccctccagagcagctgtggaaggagagacccagccggga 275
 Db 181 CAATGTGTCTTCAATGTGAGCAGCTCCAGGCCGACTGTGTGGAGGGAGACACACCCGAGG 240
 Oy 276 acgttggagacagagtgacagcagctgtgcaagccctgtgtgtgagagcagctgacccctg 335
 Db 241 ACGTGGAGACAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGC 300
 Oy 336 cctgtgacagcagcacaactctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 395
 Db 301 CCTGTGACAGACCAACTTCTCTGT 360
 Oy 396 cgtgtccttctgagcagcagctgt 455
 Db 361 GGTGTCTCTGT 420
 Oy 456 cctgtgcccctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 492
 Db 421 CCTGTGCCCTTCCAGCCACAGCAGTCCACAGCAATGTGT 457

RESULT 3
 B1824342 741 bp mRNA linear EST 04-OCT-2001
 LOCUS B1824342 603040762P1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:518130 5',
 DEFINITION B1824342
 ACCESSION B1824342
 VERSION B1824342.1 GI:15935892
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 741)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM11453 row: k column: 15
 High quality sequence stop: 731.

FEATURES

Source

1. /741
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1ib="IMAGE:5181830"
 /clone_1ib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

BASE COUNT

163 a 238 c 205 g 135 t

ORIGIN

Query Match

Best local Similarity 80.3%; Score 395; DB 10; Length 741;
 Matches 479; Conservative 0; Mismatches 10; Indels 8; Gaps 7;

QY 1 acacctgtctcgagaccacacacagctgacacgtcctcagttagaagacacaaagacccc 60
 DB 227 ACACCTGTCTCGAGACACACACAGCTGCCAGTCCCTCAGTTAGAACACAAAGACCCC 286
 QY 61 tg-ccccccacacccccagttgtccagagcagtaagcagttgtccagcatttgaaatgac 119
 DB 287 TGTCCCTCCACCCACCCCACTGTTCACAGCACTAACCACTGTCCACCACTTGGAAAGTAC 346
 QY 120 ctggcagagtgtaagtgcacatgaaatgaacgcctgagcttaccctgtgtgacctgac 179
 DB 347 CTGGCCAGAGAGTGGAACTGCACTGAATGSAAGCTGACCTTATCCTGTGTGGCTTCAG 406
 QY 180 cgcgtccccaactcaacatcctctactgctgctgagcaatggttctcttcaatgagcaact 239
 DB 407 CCGCTTCCCACTCAGCATCTCTACTGTGCGCAATGATGTCCTTCATTGAGCACT 466
 QY 240 cccagggcgaactgtggaaggagacccagccgggaacgtggagacacagatgcagc- 298
 DB 467 CCCAGGCCGACTGTGGAGGGAGACCAAGCCGGGAACGTGGAGACACAGTACGCAACT 526
 QY 299 tctgcaagagcctgtgtctgagcagctgacccctgcccgtgcaagacacacacttctcct 358
 DB 527 TGTGCAAGGCTTGTGTCTGTGAGCAGCTGACACTG-CCGTGCAAGCAGACCAACTTCTCT 565
 QY 359 gttgtcgttgaagccctgaaacaggtgtcagcgttcaagtcctgtgcccagctc--tg 416
 DB 586 GTGTGCTCGTGACCTGAAACAGG-TGTCCAGGCTACGTCGTCGCCGGCCACCATGTG 644
 QY 417 ggtctggctgagggcaactt-gccccccacccaagaagcctt-gcccttcagcacaagc 474
 DB 645 GCTGGGCTTGTAGGGCAACTTGTGGCCCCCAACCAAGAAAGCCCTTGCCCTCACACAGC 704
 QY 475 agtcccaagcagcagag 491
 DB 705 AGTCCACAGCAGCAGGG 721

RESULT

4

BI521608
 LOCUS 727 bp mRNA linear EST 29-AUG-2001
 DEFINITION 603081449F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5220396 5',
 mRNA sequence.
 ACCESSION BI521608
 VERSION BI521608.1 GI:15346400
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM11554 row: b column: 13
 High quality sequence stop: 685.

FEATURES

Source

1. /727
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1ib="IMAGE:5220396"
 /clone_1ib="NIH_MGC_120"
 /lab_host="DH10B"

BASE COUNT

159 a 218 c 209 g 141 t

ORIGIN

QY 1 acacctgtctcgagaccacacacagctgacacgtcctcagttagaagacacaaagacccc 60
 DB 244 ACACCTGTCTCGAGACACACAGCTGCCAGTCCCTCAGTTAGAACACAAAGACCCC 303
 QY 61 tgcctccccaagccccagttgtccagcagcagcagcagcagcagcagcagcagcagcagcagc 120
 DB 304 TGCCTCCCAAGCCCCCAAGTCTTCCACAGCACTGAAGAGTCCAGCATTTGGAAGTACG 363
 QY 121 tggcagaggttgaaagtgcacactgaatgaaagcgtgagctatcc-tgtgtgacctgac 179
 DB 364 TGGCAAGAGTGGAAAGTGCACACTGAATGAAACGCTGAGCACTTATCCGTGTGGCTTCAG 423
 QY 180 cgcgtccccaactcaagatcctctctgtgtgtgtggaatggttcttcaatggacact 239
 DB 424 CCGCTTCCCAACTTTAGCACTTCTTACTGCTGTGGCAAGTGGTCTTCATTGAGCACT 483
 QY 240 cccagcgcagactgtggaaggagacacacagccgggaacgtggagacacagcagcagcagcagc 299
 DB 484 CCCAGGCCAAGTGTGGAGGGAGACACACCGGGAACGTGGAGACACAGTACGCAAGCT 543
 QY 300 gtgcaagcctgtgtctgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 359
 DB 544 GTCAAGGCTTGTGTGTGTGAGCAGCTGACCCCTGCTGCACAG-ACCAACTTCTCTG 602

QY 360 tttgtctgttgagacccctgaacaggtgttcagcgttcacgttcctcctggccacgtctggac 419
|||||
Db 603 tttgtctgttgagacccctgaacaggtgttcacgttcacgttcctcctggccacgtctggac 662
QY 420 tggg 423
||
Db 663 GAGG 666

RESULT 5
B1829728 785 bp mRNA linear EST 04-OCT-2001
LOCUS B1829728
DEFINITION 603079792P1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5171399 5',
mRNA sequence.
ACCESSION B1829728
VERSION B1829728.1 GI:15941278
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 785)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L1AM1426 row: h column: 24
High quality sequence stop: 507.
Location/Qualifiers
1..785
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5171399"
/clone_id="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH-MGC library."

BASE COUNT 203 a 242 c 219 g 121 t
ORIGIN

Query Match 78.9%; Score 388.4; DB 10; Length 785;
Best Local Similarity 98.3%; Pred. No. 1.4e-79;
Matches 403; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 acacctctctgcagaccacacagctgcacgtcctcagttagaagacaaagacccc 60
|||||
Db 72 ACACCTGCTCTGACAGACACACAGCTGCTCCTCAGTTAGAACACAAAGACCCC 131

QY 61 tggccctccacagcccccagtggttcccgacgactaagcagtggtccagcattggaatgacc 120
|||||
Db 132 TGCCCTTCGCCGCCGAGGTGTTCCAGACACTAAGCAGTGTCCAGCATTTGGAAGTGACC 191

QY 121 tggcagagtgtagaagtgccacatgaatgaacgttgactatcctgtgtgctgcagc 180
|||||
Db 192 TGCGCAGAGGTGGAAGTGCCACCTGAATGGAAGCTGAGCTTATCTGTGTGCTGACGC 251

QY 181 cgcctccccaactcaagcactcctctactcgtcgtgggaatggttctctcatctagacacc 240
|||||
Db 252 CCTTCCCAACTGACATCTCTACTGCTGAGCAATGTTCTCTTCAATGAGCACCTC 311

QY 241 ccagggccagctgttggaaggagggacccagccgggaacgtgggaagacagatccagcgtg 300
|||||
Db 312 CCAGGCCGAGCTGTGGAGGGAGACACAGCCGGGAGAGCTGGAGCAGAGTACGACGTG 371

QY 301 tgaagccttggtgtcgtgagcagctgaaccctgtccctgacag--caccactctctg 359
|||||
Db 372 TGCAGGCGCTGTGCTGTGAGCAGCTGACCCCTGCCCTTCACAGACACCACTTCTCTG 431

QY 360 tttgtctgttgagacccctgaacaggtgttcacggttcacgttcctcctggccc 409
|||||
Db 432 TGTGCTGTGAGACCCGTGAACAGGTGTGTCACAGCTGACGTGCTGCTGCCC 481

RESULT 6
AM393182/c 545 bp mRNA linear EST 04-FEB-2000
LOCUS AM393182
DEFINITION CM2-ST0284-061299-046-a08 ST0284 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM393182
VERSION AM393182.1 GI:6897841
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 545)
AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l1-CM2&t2-CM2-ST0284-061299-046-a08&t3-1999-12-06&t4-1>)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 501.
Location/Qualifiers
1..545
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="ST0284"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 104 a 156 c 177 g 108 t
ORIGIN

Query Match 77.4%; Score 381; DB 9; Length 545;
Best Local Similarity 100.0%; Pred. No. 6.5e-78;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 gaagtaccttgagcagagtggaagtgccactgatgaacgtgagacttactctgtgtg 171
|||||
Db 532 GAAGTGACCTGCGCCAGAGGTGGAAGTGGCCACTGAATGGAACGCTGAGCTTATCTGTGTG 473

QY 172 gccctgacgcgcgtctcccaactcaccatccatccatctactgctggtggcaatggttccctcatt 231
 |||||||
 Db 472 GCGTCGAGCGCGTCCCAACTCAGACATCCTTACTGGCTGGCAATGTTCTTCATT 413
 |||||||
 QY 232 gagacctcccaagccgaactgtggaaggagaccagccgggaacgttggagacaggt 291
 |||||||
 Db 412 GACACACTCCCAAGCCGACGTGTGGAGGGAGCACCAGCGGGAGACGTGGAGACACAGGT 353
 |||||||
 QY 292 accgacacttgcgaagccctgtgtgtggaagcctaacccctcccttcagacagcaaac 351
 |||||||
 Db 352 ACCGACACTGTGCAAGGCTTGTGTGAGACAGCTGACCCCTGCTGCAACAGCACCAC 293
 |||||||
 QY 352 ttctcctgtgtcgtctggaaccctgaacaggtgttcacagtcagtcgtccctggccag 411
 |||||||
 Db 292 TTCTCCTGTGTGCTGTGAGCCCTGAACAAGTGTCTCAGGTACGTCTGCTGGCCAG 233
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 QY 412 ctctggctgtggtgaggaacaccttgcccccacccaagaagccctgcctccacagca 471
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 Db 232 CTCTGGGCTGTGGGTGAGGCAACCTTGCCCCACCACCAAGAGCCTGCGCTTCAGCCAC 173
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 QY 472 agcaatccacaagcagcaggt 492
 |||||||
 Db 172 AGCAGTCCACAGCAGCAGGT 152

RESULT 7
 BF375599/c 530 bp mRNA linear EST 24-NOV-2000
 LOCUS BF375599
 DEFINITION CM2-ST0284-061299-046-g02 ST0284 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF375599
 VERSION BF375599.1 GI:11337624
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bais,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?rl=CM2&rl2=CM2-ST0284-061299-046-g02&rl3=1999-12-06&rl4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 10
 High quality sequence stop: 58.

FEATURES

source 1..530
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ST0284"
 /dev_stage="Adult"
 /note="Organ: stomach; Vector: puc18; Site1: Sma1; Site2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 95 a 152 c 169 g 114 t
 ORIGIN

Query Match 77.1%; Score 379.4; DB 10; Length 530;
 Best Local Similarity 99.7%; Pred. No. 1.5e-77;
 Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 112 gaagtaacctgycacagagtgtgaagtgtccactgaatgaacgcgtgagctatcctgtgtg 171
 |||||||
 Db 515 GAAGTGAACCTGGCCAGAGGTGAAGTGCACCTGAATGAAACGCTGACCTATCCTGTGTG 456
 |||||||
 QY 172 gccctgacgcgcgtctcccaactcaccatccatccatctactgctggtggcaatggttccctcatt 231
 |||||||
 Db 455 GCGTCGAGCGGCTTCCCAACTTCAGATTCCTTACTGCGCTGGCAATGTTCTTCATT 396
 |||||||
 QY 232 gagacactcccaagccgaactgtggaaggagaccagccgggaacgttggagacaggt 291
 |||||||
 Db 395 GACACACTCCCAAGCCGACGTGTGGAGGAGCAACAAGCCGGAGACTGGGAGCACAGGT 336
 |||||||
 QY 292 accgacacttgcgaagccctgtgtgtggaacaccttgcccccacccaagaagccctgcctccacagca 351
 |||||||
 Db 335 ACCGACACTGTGCAAGGCTTGTGTGAGACAGCTGACCCCTGCTGCAACAGCACCAC 276
 |||||||
 QY 352 ttctcctgtgtcgtctggaaccctgaacaggtgttcacagtcagtcgtccctggccag 411
 |||||||
 Db 275 TTCTCCTGTGTGCTGTGAGCCCTGAACAAGTGTCTCAGGTACGTCTGCGCCAG 216
 |||||||
 QY 412 ctctggctgtggtgaggaacaccttgcccccacccaagaagccctgcctccacagca 471
 |||||||
 Db 215 CTCTGGGCTGTGGGTGAGGCAACCTTGCCCCACCACCAAGAGCCTGCGCTTCAGCCAC 156
 |||||||
 QY 472 agcaatccacaagcagcaggt 492
 |||||||
 Db 155 AGCAGTCCACAGCAGCAGGT 135

RESULT 8
 AL570875 635 bp mRNA linear EST 16-FEB-2001
 LOCUS AL570875
 DEFINITION AL570875 LRI_NFL006_PL2 Homo sapiens cDNA clone CSOD1012Yr15 5
 ACCESSION AL570875
 VERSION AL570875.1 GI:12927610
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source 1..635
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CSOD1012Yr15"
 /clone_lib="LRI_NFL006_PL2"
 /tissue_type="Placenta"
 /note="Vector: pCMVSPORT 6; Site1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies. Contact : Feng liang life technologies, a division of invitrogen 9800 Medical Center Drive

	Query Match	69.68;	Score 342.4;	DB 10;	length 589;
	Best Local Similarity	81.4%;	Pred. No. 5.3e-69;		
	Matches 397; Conservative	0;	Mismatches 91;	Indels 0;	Gaps 0;
OY	I acacactctccgcagaccaccaaacgtcgaatgaccttcatttagaagaacaagaacccc	60			

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5181242"
/clone_1bp="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis. Vector:
pCW-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. library is

```


OM of: US-09-786-130-1 to: EST.* out_format: pfs

Date: Aug 19, 2002 11:24 PM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-MODE=frame+pnz-model -DEV=xlh
-O=cn2_1/USPFO.spool/US09786130/runat_15082002_160056_6285/app-query.fasta_1.222
-DB=EST -QPM=fastap -SUFFIX=est -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -OGAPOP=4.500
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FCAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELCP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blissum62 -TRANS=human4.0.cdi
-LIST=45 -DOCALLGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIG=15 -MODE=LOCAL -OUTFMT=pts -NORM=ext -HEADSIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09786130.@CN1_1_2515
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPHY -WAIT -THREADS=1
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Search information block:

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Query: US-09-786-130-1
Query length: 164
Database: EST.*
Database sequences: 13736207
Database length: -1841457050
Search time (sec): 1601.550000
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score_list:

Sequence	Strd	Orig	ZScore	EScore	len	Documentation
gb_est1:AW962849	+	795.00	1300.33	3.5e-63	547	AW962849 EST374922 MAGC resequ
gb_est1:AA311795	+	773.00	1266.29	2.8e-61	451	AA311795 EST182531 Jurkat T-cell
gb_est1:BI824342	+	724.50	1181.06	1.5e-56	741	BI824342 603040762F1 NIH_MGC_11
gb_est1:BI829728	+	706.00	1150.01	8.3e-55	785	BI829728 603079792F1 NIH_MGC_11
gb_est1:BI521608	+	703.00	1145.93	4.4e-54	727	BI521608 603081449F1 NIH_MGC_12
gb_est1:AW933182	+	675.00	1103.08	3.4e-52	545	AW933182 CM2-ST0284-061299-046-
gb_est1:BF375599	+	670.00	1095.16	9.4e-52	530	BF375599 CM2-ST0284-061299-046-
gb_est1:AL570875	+	667.50	1089.06	2.1e-51	635	AL570875 LIT-NEFL006.PH
gb_est1:AW933184	+	639.00	1044.07	6.6e-49	536	AW933184 CM2-ST0284-061299-046-
gb_est1:AW933204	+	632.00	1032.22	3.0e-48	549	AW933204 CM2-ST0284-061299-046-
gb_est1:BG775971	+	628.00	1022.22	1.1e-47	754	BG775971 602650008F1 NIH_MGC_40
gb_est1:AW933201	+	625.00	1021.16	1.2e-47	515	AW933201 CM2-ST0284-061299-046-
gb_est1:BF375685	+	623.00	1016.56	2.2e-47	515	BF375685 RCS-ST0300-151299-031-
gb_est1:BI828272	+	599.50	973.39	5.7e-45	901	BI828272 603040310F1 NIH_MGC_11
gb_est1:AW933194	+	594.00	970.04	8.7e-45	538	AW933194 CM2-ST0284-061299-046-
gb_est1:BI961303	+	584.00	952.60	1.2e-44	589	BI961303 MONO1_8_F10.B1-A005 MG
gb_est1:BF375600	+	546.00	892.79	1.8e-40	463	BF375600 CM2-ST0284-061299-046-
gb_est1:BI153483	+	519.00	844.38	8.7e-38	666	BI153483 602915551F1 NCI_CGAP_1
gb_hlc:AK009721	+	515.00	831.08	4.8e-37	1224	AK009721 Mus musculus adult ma
gb_hlc:AK003370	+	515.00	830.29	5.3e-37	1314	AK003370 Mus musculus 18 days
gb_hlc:AK008432	+	515.00	830.13	5.4e-37	1334	AK008432 Mus musculus adult ma
gb_est1:BI961303	+	512.00	813.79	3.4e-37	613	BI961303 MONO1_8_F10.B1-A005 MG
gb_est1:BE200246	+	503.00	818.07	2.5e-36	666	BE200246 ug61h10.x1 Soares_mamm
gb_est1:AW933202	+	481.00	790.17	9.1e-35	315	AW933202 CM2-ST0284-061299-046-
gb_est1:AW933180	+	479.50	783.26	2.2e-34	471	AW933180 CM2-ST0284-061299-046-
gb_est1:BE381966	+	479.50	779.13	3.8e-34	685	BE381966 601271915F1 NCI_CGAP_1
gb_est1:BF375597	+	478.50	783.40	8.2e-34	401	BF375597 CM2-ST0284-061299-046-
gb_est1:AW933187	+	470.00	773.06	8.2e-34	451	AW933187 CM2-ST0284-061299-046-
gb_est1:BG864668	+	471.00	765.41	2.8e-33	802	BG864668 602798384F1 NIH_CGAP_1
gb_est1:AA980066	+	468.50	763.49	2.2e-33	458	AA980066 ua28b09.r1 Soares_mamm
gb_est1:BF724662	+	465.00	761.62	3.6e-33	386	BF724662 bx07d09.y1 Human T1S
gb_est1:AT227465	+	445.50	727.27	4.9e-31	475	AT227465 U10a03.y1 Soares_mamm
gb_est1:AW933185	+	443.50	705.30	4.9e-30	482	AW933185 CM2-ST0284-061299-046-
gb_est1:BE448456	+	369.50	601.80	2.8e-24	498	BE448456 uc9b007.y1 Soares_mamm
gb_est1:BE137302	+	355.50	579.35	5.1e-23	473	BE137302 uc9b107.y1 Soares_mamm
gb_est1:BI824811	+	332.00	537.15	1.1e-20	653	BI824811 60303712F1 NIH_MGC_11
gb_est1:AW227321	+	308.50	503.10	8.9e-19	431	AW227321 up10e06.y1 NCI_CGAP_11
gb_est1:AK009877	+	302.50	496.49	2.1e-18	321	AK009877 Mus musculus adult ma
gb_est1:BF220561	+	279.00	488.28	6.0e-18	401	BF220561 QV0-NT0150-081100-454-
gb_est1:AW962849	+	271.00	444.70	1.6e-15	321	AW962849 CM2-ST0284-061299-046-

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gb_est1:BF375598 + 260.00 430.89 9.4e-15 218 | BF375598 CM2-ST0284-061299-
gb_est1:AV092729 + 254.00 404.12 2.9e-13 1007 | AV092729 AV092729 Mus musc
gb_est1:AA498857 + 245.00 399.12 5.5e-13 447 | AA498857 v182b02.r1 Strata
gb_est1:BE200242 - 232.50 378.65 7.6e-12 412 | BE200242 ug61h04.x1 Soares_
gb_est1:AA297872 + 225.00 369.11 2.6e-11 320 | AA297872 EST113437 Jurkat T
seq_name: gb_est1:AW962849
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seq_documentation block:

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LOCUS AW962849 547 bp mRNA linear EST 01-JUN-2000
DEFINITION EST374922 MAGC resequenes, MAGC Homo sapiens cDNA, mRNA sequence.
ACCESSION AW962849
VERSION AW962849.1 GI:8152685
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 547)
Hegde,P., Ol,R., Abernathy,K., Dharap,S., Gasparid,R., Gay,C., Holt
I.E., Speed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
CONTACT: John Quackenbush
JOURNAL The Institute for Genomic Research
COMMENT 9112 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johng@tigr.org
Plate: 180
Seq primer: Reverse.
```

FEATURES

```
source Location/Qualifiers
1..547 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGC resequenes, MAGC"
/note="Vector: pBluescriptSKm"
BASE COUNT 115 a 183 c 145 g 104 t
ORIGIN
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alignment_scores: 795.00 Length: 152
Ratio: 5.300 Gaps: 0
Percent Similarity: 98.684 Percent Identity: 98.026
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alignment_block:
US-09-786-130-1 x AW962849 ..

Align seg 1/1 to: AW962849 from: 1 to: 547

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13 seryAlaGserThlyAspProCyProSerGlnProValPhePr 29
2 TCAGTGTAGAACGACAAAGACCCCTGCCCTCCAGCCCAAGTTC 51
29 CALAAlaGlyGlnGlyProAlaLeuGluValThrTrpProGluValGluV 46
52 AGCAGCTAACGAGTCTCCAGCATTTGAGATGACCTGGCCAGAGTGAAG 101
46 alProLeuAsnGlyThrLeuSerLeuSerCysValAlaCysSerArgPhe 62
102 TGCCCACTAAATGGAACGCTGAGCTTATCTGTGTGGCTGCAAGCCGCTTC 151
63 ProAsnPheserIleLeuTyTrpLeuGlyAsnGlySerPheIleGluNI 79
152 CCCAACTTACGACATCCCTACTGCTGGCGCAATGGTTCCTTCATGAGCA 201
79 sleuProGlyArgLeuTrpGluGlySerThrSerArgGluArgGlySerT 96
202 CCTCCAGGCGGAGCTGTGGAGGAGGACACGACCGGAGACGTGGAGACA 251
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352 CCAGCGTCAGCTGCTGGCCCACTGCGCTGGGCTGAGGCAACCT 401
 146 eupProthrGlnGlnAlaLeuProSerSerHisSerProGlnGln 162
 402 TGCCCCCAACCAAGAGCCCTGCTCCAGCCACAGTCACAGCA 451
 163 GlnGly 164
 452 CATGGT 457
 seq_name: gb_est1:AA311795

seq_documentation_block:

LOCUS AA311795 451 bp mRNA linear EST 19-APR-1997
 DEFINITION EST182531 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to
 similar to Hypothetical protein C9, mRNA sequence.

ACCESSION AA311795

VERSION AA311795.1 GI:1964144

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 451)

REFERENCE

AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fudner, R.A., Bult,
 C.J., Lee, N.H., Kirkness, E.F., Weissstock, K.G., Gocayne, J.D., White,
 O., Sutton, G., Blake, J.A., Brandon, R.C., Man, Wai, C., Clayton, R.A.,
 Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald,
 L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S., Glodek, A.,
 Ghehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,
 Kelley, J.C., Liu, L.-I., Marra, S.M., Merrick, J.M.,
 Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Peligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
 Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
 Bednarek, D.P., Cao, B., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
 Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,
 Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
 Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L.,
 Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon,
 M.R., Rosen, C.A., Haseilane, W.A., Fields, C., Fraser, C.W., and
 Venter, J.C.

TITLE

Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence

JOURNAL

MEDLINE

COMMENT

Other ESTs: TRC123801

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse

FEATURES

Source

1. .451
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):159026"
 /db_xref="taxon:9606"
 /clone_id="Jurkat T-cells VI"

/cell_type="T-lymphocyte"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 88 a 152 c 126 g 83 t 2 others
 ORIGIN

alignment_scores:

Quality: 773.00 Length: 149
 Ratio: 5.295 Gaps: 0
 Percent Similarity: 97.987 Percent Identity: 97.987

alignment_block:

US-09-786-130-1 x AA311795 ..

Align seg 1/1 to: AA311795 from: 1 to: 451

13 SerValArgSerThrIysAspProCysProSerGlnProProValPheP 29
 3 TCAGTTAGAAAGCACAAAGACCCTGCTCCCTCCACAGCCAGCTTCC 52
 29 GAlaAlaLysGlnCysProAlaLeuGlnValThrTrpProGluValGluV 46
 53 AGCAGCTAAGCAAGTGTCCAGATTGGAAGTGAAGTGAAGTGAAG 102
 46 aLProLeuasnGlyThrLeuSerLeuSerCysValAlaCysSerArgPhe 62
 103 TGCCACTGAATGGAACGCTGAGCTTATCTGCTGCTGCTGACCCCTTC 152
 63 ProAsnPheserThrLeuGlyTrpLeuGlyAsnGlySerPheLeuH 79
 153 CCCAACTTCAGCAATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 202
 79 sleuProGlyArgLeuTrpGlnGlySerThrSerArgGluArgGlySer 96
 203 CTTCCAGGCGGCGACTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 252
 96 hreGlyThrGlnLeuGlyValAlaLeuValLeuGlnGlnLeuThrProAla 112
 253 CAGGTACGACGAGTGTCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTG 302
 113 LeuHisSerThrAsnPheserCysValLeuValAspProGlnGlnVal 129
 303 CTGCACAGCAACCACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 352
 129 LglnArgHisValValLeuAlaGlnLeuTrpAlaGlyLeuArgAlaThrL 146
 353 CCAGCGCTNCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 402
 146 eupProThrGlnGlnAlaLeuProSerSerHisSerProGln 161
 403 TGCCGCCACCAACCAAGAGCCCTGCTCCAGCCACAGCAGCTCCACAG 449
 seq_name: gb_est2:BI824342

seq_documentation_block:

LOCUS BI824342 741 bp mRNA linear EST 04-OCT-2001
 DEFINITION 603040762F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5181830 5',
 mRNA sequence.

ACCESSION BI824342

VERSION BI824342.1 GI:15935892

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 741)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Comment: cgaps-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L14M1453 row: k column: 15
 High quality sequence stop: 731.

FEATURES

source

Location/Qualifiers

1..741

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:518130"

/clone_lib="NIH_MGC_115"

/lab_host="DH10B"

/note="Organ: pooled brain, lung, testis; Vector:
 PCMV-SPORE6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

BASE COUNT 163 a 238 c 205 g 135 t
 ORIGIN

alignment_scores:

Quality: 724.50 Length: 168

Ratio: 4.500 Gaps: 4

Percent Similarity: 95.833 Percent Identity: 92.262

alignment_block:

US-09-786-130-1 x B1824342 ..

Align seg 1/1 to: B1824342 from: 1 to: 741

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1  ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerTh 17
|||||
227 ACACCTGCTGCGACACACACACACCTGCTGCTAGTAGAAGCAG 276
17  rlyAspProCys.ProSerGlnProProValPheProAlaAlaLysGln 33
|||||
277 AAAGGACCCCTGCTCCCTCCACAGCCCAAGTGTTCACGACGCTAAGCAG 326
34  CysProAlaLeuGluValThrTrpProGluValGluValProLeuAsnG1 50
|||||
327 TGTCGAGCATGTGAAGTACCTGGGCGAGAGTGAAGTGCACCTGAATGG 376
50  yThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSer1 67
|||||
377 AACGCTGAGCTTATCTGTGTGCTGCGAGCGCTCCCAACTTCACACA 426
67  leLeuTrpTrpLeuGluYasnGlySerPheIleGluHisLeuProGluArg 83
|||||
427 TCCTCTACTGCTGGGCAATGTTCTTCATTGAGACACCTCCGACGGCGA 476
84  LeuTrpGluGlySerThrSerArgGluArgGlySerThrGlyThrGlnL 100
|||||
477 CTGTGGAGGGGAGACACACCGGGGAACGTGGAGACACAGTACGCACT 526
100  euCysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThr 116
|||||
527 TGTCAAGAGCCCTGTGTGTGAGCAGCTGCACACCTGC.CTGCACAGCAC 575
117  AsnPheSerCysValLeuValAspProGluGlnValAlaGlnArgHisVa 133
|||||
576 AACCTTCTCTGTGTGCTGCGACCTGAACAGGT.GTCCAGCGCTCAGCT 624
133  lValLeuAlaGlnLeu.TrpAlaGlyLeuArgAlaThrLeu...ProPro 148
|||||

```

625 GTCCCGCCGACAGATCATGGGCTTGAGGCGCAACCTTGCCCCCA 674
 149 ThrGlnGluAlaLeuProSerSerHisSerSerProGlnGlnGly 164
 675 ACCAAGAAAGCCCTGGCCCTCCAGCACAGCACTCCACAGCAGAGGG 722

seq_name: gb_est2:B1829728

seq_documentation_block:

LOCUS B1829728 785 bp mRNA linear EST 04-OCT-2001

DEFINITION 603079792F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:517139 5',

mRNA sequence.

ACCESSION B1829728

VERSION B1829728.1 GI:15941278

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

1 (bases 1 to 785)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: L14M1426 row: h column: 24

High quality sequence stop: 507.

FEATURES

source

Location/Qualifiers

1..785

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:517139"

/clone_lib="NIH_MGC_119"

/tissue_type="medulla"

/lab_host="DH10B"

/note="Organ: brain; Vector: PCMV-SPORE6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library"

BASE COUNT 203 a 242 c 219 g 121 t
 ORIGIN

alignment_scores:

Quality: 706.00 Length: 178

Ratio: 4.555 Gaps: 4

Percent Similarity: 87.079 Percent Identity: 80.899

alignment_block:

US-09-786-130-1 x B1829728 ..

Align seg 1/1 to: B1829728 from: 1 to: 785

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1  ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerTh 17
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72 ACACCTGCTGCGACACACACAGCTGCTGCTAGTAGAAGCAG 121
17  rlyAspProCysProSerGlnProProValPheProAlaAlaLysGln 34
|||||
122 AAAGGACCCCTGCGCCCTCCGCGCCGAGTGTCCACAGCAGCTAAGCAGT 171

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34 ysfProAlaLeuGluValThrTrpProGluValGluValProLeuAsnGly 50
|||||
172 GTCCAGCATTTGGAATGACCTGGCCAGAGGTGGAAGTGCACATGAATGCA 221
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSer1 67
|||||
222 ACCCTGAGCTTATCTGTGTGGCTGCAGCCGCTTCCCAACTTCACACAT 271
67 eleuTyrrTrpLeuGlyAsnGlySerPheIleGluHisLeuProGlyArgL 84
|||||
272 CCTCTACTGGCTGGGCAATGTTCTTCATTGAGCACTCCAGGCCGAC 321
84 euTrpGluGlySerThrSerArgGluArgGlySerThrGlyThrGluLeu 100
|||||
322 TGTGGGGGGGAGACACCGCCGGGAACGTGGAGACAGGTACGACGCTG 371
101 CysLysAlaLeuValLeuGluGluGlnLeuThrProAlaLeuHis_SerThra 117
|||||
372 TGCAGAGCCTTGCTGCTGGAGACAGTGCACCTGACCTGCGACAGACCA 421
117 snPheSerCysValLeuValAspProGluGlnValValGlnArgHisVal 133
|||||
422 ACTTCTCCTGTGTGCTGTGGACCTGGAACAGTTGTCCAGCGTCACGTC 471
134 ValLeuAlaGln...LeuTrpAlaGlyLeuArg..... 143
|||||
472 GGTCTGGGCCCAAGCTGTGAGCCTGGGCTGGAAGGCGCAAACTTGCC 521
144 .....AlaThrLeuProProThrGlnGluAlaLeuPro 154
|||||
522 CCCGCAAGCCCAAGAAATGCCACTTGGCCCCCTCCCAAGGACAGAGCAC 571
155 SerSerHisSerSerProGlnGlnGlnGly 164
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572 GGGATTACACACAGAAAGACCAAAATGGC 601
seq_name: gb_est2:B1521608

seq_documentation_block:
LOCUS B1521608 727 bp mRNA linear EST 29-AUG-2001
DEFINITION 603081449F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5220396 5',
ACCESSION B1521608
VERSION B1521608.1 GI:15346400
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 727)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LHAM1554 row: b column: 13
High quality sequence stop: 685.
location/Qualifiers
1..727
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5220396"
/clone_id="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector:
pcmv-sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
```

```
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH-MGC library."

BASE COUNT 159 a 218 c 209 g 141 t
ORIGIN

alignment_scores:
Quality: 703.00 Length: 150
Ratio: 4.916 Gaps: 1
Percent Similarity: 95.333 Percent Identity: 92.667

alignment_block:
US-09-786-130-1 x B1521608 ..

Align seg 1/1 to: B1521608 from: 1 to: 727

1 ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerTh 17
|||||
244 ACACCTGTCTCGCAGACACACACAGCTGCCACTGCTCAGTTAGAACAC 293
17 rlyAspProCysProSerGlnProValPheProAlaAlaLysGlnC 34
|||||
294 AAGAGACCCCTGCCCTCCAGCCCCAGTGTCCAGCAGTAAACAGT 343
34 ysfProAlaLeuGluValThrTrpProGluValGluValProLeuAsnGly 50
|||||
344 GTCCAGCATTTGGAATGACCTGGCCAGAGGTGGAAGTGCACATGAATGA 393
51 ThrLeuSerLeuSer CysValAlaCysSerArgPheProAsnPheSer1 67
|||||
394 ACCCTGAGCTTATCTGTGTGGCTGCAGCCGCTTCCCAACTTACGA 443
67 leuTyrrTrpLeuGlyAsnGlySerPheIleGluHisLeuProGlyArgL 83
|||||
444 TCCTCTACTGGCTGGGCAATGTTCTTCATTGAGCACTCCAGGCCGA 493
84 LeuTrpGluGlySerThrSerArgGluArgGlySerThrGlyThrGln 100
|||||
494 CTGTGGAGGGGAGACACAGCCGCGGAACGTGGGAGACAGTACGACGCT 543
100 uCysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThra 117
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544 GTCCAGAGCCTTGCTGTGCTGAGACGCTGACCCCTGCGTCGACAG. ACCA 592
117 snPheSerCysValLeuValAspProGluGlnValValGlnArgHisVal 133
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593 ACTTCTCCTGTGTGCTGTGGACCTGGAACAGTTGTCCAGCGTCACGTC 642
134 ValLeuAlaGlnLeuTrpAlaGlyLeuArgAlaThrLeuProProThr 149
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seq_name: gb_est1:AW393182

seq_documentation_block:
LOCUS AW393182 545 bp mRNA linear EST 04-FEB-2000
DEFINITION CW2-ST0284-061299-046-a08 ST0284 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW393182
VERSION AW393182.1 GI:6897841
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 545)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
unpublished (1999)
```

COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=CM2&l2=CM2-ST0284-
061299-046-208&t3=1999-12-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 501.
Location/Qualifiers
1. 545
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0284"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 104 a 156 c 177 g 108 t
ORIGIN
alignment_scores:
Quality: 675.00 Length: 127
Ratio: 5.315 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-786-130-1 x AM393182/rev ..
Align seg 1/1 to reverse of: AM393182 from: 1 to: 545
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532 GAAGTGACCTGGCCAGAGTGGAAGTCCACTGATGAGACGCTGAGCTT 483
54 uSerCysValAlaCysSerArgPheProAsnPheserIleuTyrrPL 71
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482 ATCTGTGTGGCTGCACGCCCTTCCCACTTCAGCATCTCTACTGGC 433
71 euGLyAsnGLySerPheIleGluHisLeuProGlyArgLeuTrpGlnGly 87
|||||
432 TGGGCAATGGTCTCTTCAATTAGACACCTCCAGGCGGAGCTGGGAGGG 383
88 SerThrSerArgGluArgGlySerThrGlyThrGlnLeuCysLysAlaLe 104
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382 AGCACACACCGGGAACGTGGAGGACAGGTACGACGCTGCAAGGCTT 333
104 uValLeuGlnGlnLeuThrProAlaLeuHisSerThrAsnPheserCysV 121
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332 GGTGCTGGAGGAGCTGACCCCTGCCCTGCACAGACCAACTTCTCTGTG 283
121 allLeuValAspProGluGlnValValAlGlnArgHisValValLeuAlaGln 137
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282 TGCTCTGTGACCTGTGACAGAGTTGTCCAGCTCACGCTGCTGCCCCC 233
138 LeuTrpAlaGlyLeuArgAlaThrLeuProProThrGlnGlnAlaLeuPr 154
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232 CTCTGGGCTGGGCTGAGGGCAACCTGGCCCCCAACCAAGAGCCCTGCC 183
154 oSerSerHisSerSerProGlnGlnGlnGly 164
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182 CTCAGGCCACAGAGCTCCACAGCAGCAGGGT 152

seq_name: gb_est2:BF375599
seq_documentation_block:
LOCUS BF375599 530 bp mRNA linear EST 24-NOV-2000
DEFINITION CM2-ST0284-061299-046-g02 ST0284 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF375599
VERSION BF375599.1 GI:11337624
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=CM2&l2=CM2-ST0284-
061299-046-g02&t3=1999-12-06&t4=1)
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High quality sequence start: 10
High quality sequence stop: 58.
Location/Qualifiers
1. 530
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0284"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 95 a 152 c 169 g 114 t
ORIGIN
alignment_scores:
Quality: 670.00 Length: 127
Ratio: 5.276 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.213
alignment_block:
US-09-786-130-1 x BF375599/rev ..
Align seg 1/1 to reverse of: BF375599 from: 1 to: 530
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515 GAAGTGACCTGGCCAGAGTGGAAGTCCACTGATGAGACGCTGAGCTT 466
54 uSerCysValAlaCysSerArgPheProAsnPheserIleuTyrrPL 71
|||||
465 ATCTGTGTGGCTGCACGCCCTTCCCACTTCAGCATCTCTACTGGC 416

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71  euGIyasnGIySerPheIIeGIuHISLeuProGIyArGIeUTrPGIuGIy 87
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415  TGGGCAATGTTCTTCATTGAGCACCTCCACAGCCGACGTGTGGAGGG 366
88  SerThrSerArgIuArgIySerThrGIyThrGIuLeuCyStyAla 104
   |||:::|||||
365  AGCAACAGCGGGAGCGTGGGACACAGTACGACACTGTGCAGAGCCTT 316
104  uValLeuGIuGIuLeuThrProAlaLeuHISerThrAsnPhSeCysV 121
   |||||||
315  GGTGCTGGAGCAGCTGACCCCTGCTGCACACACCACTTCTCTGTG 266
121  aIleuValAspProGIuGIuValaIglArGIHISValaIleuAlaGIu 137
   |||||||
265  TGTCTGTGACCTGTGAACAGGTGTGCAGCTGCACGTCTGTGCTGCCAG 216
138  LeuTrpAlaGIyLeuArGIaTrpAlaTrpProThrGIuGIuAlaLeuP 154
   |||||||
215  CTCTGGGCTGGGCTGGAGGCGACCTTGCCCCACCCCAAGAGCCCTGCC 166
154  oSerSerHISerSerProGIuGIuGIuGIy 164
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165  CTCACAGCACAGCAGTCCACAGCAGAGGT 135

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seq_name: gb_est1:AL570875

seq_documentation_block:

LOCUS AL570875 635 bp mRNA linear EST 16-FEB-2001
 DEFINITION AL570875 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1012YF15 5
 prime, mRNA sequence.

ACCESSION AL570875
 VERSION AL570875.1 GI:12927610

KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 635)

AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
 Location/Qualifiers

FEATURES

source

1..635
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1012YF15"
 /clone_lib="LTI_NFL006.PL2"
 /tissue_type="Placenta"

/note="Vector: pCMVSPORT 6; Site 1: NotI. 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetechn.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 128 a 213 c 170 g 118 t 6 others

ORIGIN

alignment_scores:

Quality: 667.50

Length: 154

Ratio: 4.635

Gaps: 2

Percent Similarity: 93.506

Percent Identity: 91.558

alignment_block:

US-09-786-130-1 x AL570875 ..
 Align seg 1/1 to: AL570875 from: 1 to: 635

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1  ThrProValSerGIuThrThrThrAlaAlaThrAlaSerValaArgSerTh 17
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175  ACACCTGTCTCGCAGACACACACAGCTGCCAGCTGCCTCAGTTAAGAAGCAC 224
17  rIlyAsp...ProCysProSerGIuProProValPheProAlaAlaIlySg 33
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225  AAGGAGACGCCCTGGCCCTCCAGGCCAGGTTCCAGCAGCAGTAAAG 274
33  IncysProAlaLeuGIuValaThrTrpProGIuValaGIuAlaProIleAsn 49
   |||||||
275  AGTGTCCAGATTGGAAGTACCTGGCCAGAGGTGAAGTGCACACAGAAT 324
50  GIYThrLeuSerSerSerCysValaIaCysSerArgPheProAsnPhSe 66
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325  GGACGC CTGAGCTTATCTGTGTGTGGCTTGACGCGCTTCCCAACTTCAAG 373
66  rIleuTrpGIyTrpLeuGIyAsnGIySerPheIIeGIuHISLeuProGIyA 83
   |||||||
374  CATCTCTACTGTGGCTGGCAATGTTCCTTCATTGAGCACCTGCCAGGCC 423
83  rGIeUTrPGIuGIySerThrSerArgGIuArgIySerThrGIyThrGIu 99
   |||||||
424  GACTGTGGAGGGGAGCACACCGGGGAACGTGGGAGCACAGGTACGACAG 473
100  LeuCyStyAlaLeuValLeuGIuGIuGIuLeuThrProAlaLeuHISerTh 116
   |||||||
474  CTGTGCAGAGCCCTTGCTGCTGCAGACGACGACCCCGGCCGNCACANCMAC 523
116  rAsnPhSeSerCysValaLeuValaAspProGIuGIuValaIglArGIHISV 133
   |||||||
524  CAACCTCTCTCTGTGTGTGTGGGAGCTGACACAGT. GTCCAGCGCACAG 572
133  aIValLeuAlaGIuLeuTrpAla.GIyLeuArGIaThrLeuProThr 149
   |||||||
573  TGTCTCTGGCCAGCTGTGGGCTGAGGTTGAGGGCACAACCTTGCCCCCAC 622
149  rGIuGIuAla 152
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623  CCAGAAGGCC 632

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seq_name: gb_est1:AW393184

seq_documentation_block:

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 DEFINITION CM2-ST0284-061299-046-a11 ST0284 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW393184

VERSION AW393184.1 GI:6897843

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 536)

AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cli=CM2&t2=CM2-ST0284-
 061299-046-a11&t3=1999-12-06&t4=1)
 Seq primer: puc 18 forward

High quality sequence start: 9
High quality sequence stop: 536.
Location/Qualifiers
1..536

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/organism="Homo sapiens"
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/clone_lib="ST0284"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site.1: Sma1;
Site.2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 105 a 150 c 172 g 109 t
ORIGIN

alignment_scores:

Quality: 639.00 Length: 128
Ratio: 5.112 Gaps: 1
Percent Similarity: 97.656 Percent Identity: 96.875

alignment_block:
US-09-786-130-1 x AW393184/rev ..

Align seg 1/1 to reverse of: AW393184 from: 1 to: 536

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38 GluValThrTrpProGluValGluValProLeuAsnGlyThrLeuSerLe 54
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54 uSerCysValAlaCysSerArgPheProAsnPheSerIleLeuTyrrPl 71
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471 ATCTGTGTGGCTGCAGCCGCTTCCCACTGACATCTCTACTGTCTC 422
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71 euGlyAsnGlySerPheIleGluHisLeuProGlyArgLeuTrpGluGly 87
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421 TGGGCATATGCTTCTTCATTGAGCACCCTCCAGGCCAGCTGTGGAGGG 372
   |||||||
88 SerThrSerArgGluArgGlySerThrGlyThrGln.LeuCysLysAla 104
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371 AGCACCGACCGGGAACGTGGGAGCAGAGGTACGACGTTGTGCAAGGCT 322
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104 euValLeuGluGlnLeuThrProAlaLeuHisSerThrAsnPheSerCys 120
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321 TGGTTGTGGAGCAGCTGACCCCTGCTGCACAGCACCACCACTTCTCCT 272
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121 ValLeuValAspProGluGlnValValGlnArgHisValValLeuAlaG 137
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271 GTGCTGTGGAGCCTGAACAGGTGTCCAGAGTCACGTCCTCGGCCCA 222
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137 nLeuTrpAlaGlyLeuArgAlaThrLeuProProThrGlnGluAlaLeu 154
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221 GCTCTGGGCTGGGCTGAGGGCAACCTTGCCCCACCAAGAACCCCTGC 172
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154 roSerSerHisSerSerProGlnGlnGlnGly 164
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seq_name: gb_est1:AW393204

seq_documentation_block:

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ACCESSION AW393204
VERSION AW393204.1 GI:6897863
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 549)
AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tbl=CM2&tbl2=CM2-ST0284-061299-046-906&tbl3=1999-12-06&tbl4=1>)
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High quality sequence start: 20
High quality sequence stop: 71.
Location/Qualifiers

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1..549
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/clone_lib="ST0284"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site.1: Sma1;
Site.2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 108 a 154 c 175 g 112 t
ORIGIN

alignment_scores:

Quality: 632.00 Length: 129
Ratio: 5.056 Gaps: 2
Percent Similarity: 96.899 Percent Identity: 96.124

alignment_block:
US-09-786-130-1 x AW393204/rev ..

Align seg 1/1 to reverse of: AW393204 from: 1 to: 549

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54 uSerCysValAlaCys.SerArgPheProAsnPheSerIleLeuTyrrTrp 70
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470 ATCTGTGTGGCTGCATCCGCTTCCCTACTGACATCTCTACTGTG 421
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   |||||||
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87 ySerThrSerArgGluArg.GlySerThrGlyThrGlnLeuCysLysAla 103
   |||||||
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104 LeuValLeuGluGlnLeuThrProAlaLeuHisSerThrAsnPheSerCys 120
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120 sValLeuValAspProGluGlnValValGlnArgHisValValLeuAlaG 137
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137 nLeuTrpAlaGlyLeuArgAlaThrLeuProProThrGlnGluAlaLeu 153
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154 ProSerSerHisSerProGlnGlnGlnGly 164
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170 CCTCCAGCCACAGCAGCTCCACAGCAGAGGT 138

seq_name: gb_est2:B6775971

seq_documentation_block:
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DEFINITION 602650008F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:4761073 5',
            mRNA sequence.
ACCESSION  B6775971
VERSION    B6775971.1  GI:14046288
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 754)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: rgs@bbs-rtmail.nih.gov
            Tissue Procurement: DCTD/DTF
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: L16M1612 row: p column: 02
            High quality sequence stop: 653.
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                /clone="IMAGE:4761073"
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                /lab_host="DH10B (phage-resistant)"
                /note="Organ: prostate; Vector: pOT7; Site_1: XhoI;
                Site_2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Library constructed by
                Ling Hong in the laboratory of Gerald M. Rubin (University
                of California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library."
BASE COUNT  174 a      242 c      196 g      142 t
ORIGIN
alignment_scores:
    Quality: 628.00      Length: 155
    Ratio: 4.361      Gaps: 3
    Percent similarity: 92.903      Percent identity: 90.968

alignment_block:
US-09-786-130-1 x B6775971 ..

Align seg 1/1 to: B6775971 from: 1 to: 754

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185 ACACCTGCTGCAGACACACACAGCTGCCTCCTCAGTTAAGAACAC 234

17  rLysAspProCysProSerGlnProProValPheProAlaAla..LysG 33
|||||
235 AAAGACCCCTGCCCCCTCCACAGCCCAAGTGTCCACAGAGCTAAGGCA 284

33  ncGySProAlaLeuGluValThrTrrProGluValGluValProLeuAsnG 50
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285 GTGTCCAGCATTTGGAAAGTAGCCTGGCCACAGAGTGGAATGCCACTGATG 334
50  lYThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSer 66
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335 GAAGCGTAGAGCTTATCCCTGTGTGGCTGCAGCGG. TTCCCAACTTCACG 383
67  lLeuTyrTrrProGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 83
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384 ATCCCTTACTGCTGGCGGCAATGATGCTTCATTTGACACCTCCACAGCGCA 432
83  gleuTrrpGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
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433 .CTGTGGAGGAGGAGCACCACCGGGAACCTGGGAGCAGACAGTACGTCAC 482
100 euCysLysAlaLeuValLeuGluGlnLeuThrProAla...LeuHisSer 115
|||||
483 TGTGCAGAGC. TTGGTGTGTGAGACAGCTGACACCTTGACCTGCAGCAGC 531
116 ThrAsnPhSerCysValLeuValAspProGluGlnValValGlnArg.. 131
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532 ACCAACTTCTCCTGTGTGCTGCTGGACCTGAAACAGAGTGTCCAGAGTCA 581
132 .HsValValLeuAlaGlnLeuTrrAlaGlnLeuArgAlaThrLeuProp 148
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582 AGGTCCGCTCTGCGCCACAGCTGTGGCTGGATGAGGGCACTTGCCCCC 631
148 roThrGlnGlnAla 152
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632 CACACCAAGAACGCC 645

seq_name: gb_est1:AM393201

seq_documentation_block:
LOCUS      AM393201          531 bp      mRNA      linear      EST 04-FEB-2000
DEFINITION CM2-ST0284-061299-046-f05 ST0284 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AM393201
VERSION    AM393201.1  GI:6897860
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 531)
AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
TITLE     The FAPESP/LICR Human Cancer Genome Project
JOURNAL   Unpublished (1999)
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&lt2=CM2-ST0284-
            061299-046-f05&lt3=1999-12-06&lt4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 14
            High quality sequence stop: 337.
            Location/Qualifiers
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="ST0284"
                /dev_stage="Adult"
                /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
                Site_2: SmaI; A mini-library was made by cloning products
                derived from ORESTES PCR (U.S. Letters Patent application
                No. 196,716 - Ludwig Institute for Cancer Research)
                profiles into the puc 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under

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BASE COUNT 103 a 149 c 169 g 110 t
ORIGIN

alignment_scores:

Quality: 625.00 Length: 128
Ratio: 5.040 Gaps: 1
Percent Similarity: 96.875 Percent Identity: 96.094

alignment_block:

US-09-786-130-1 x AW393201/rev ..

Align seg 1/1 to reverse of: AW393201 from: 1 to: 531

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38  GluValIhTrrTPProGluValIgluValProLeuAaNglyThLeuSerLe 54
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530  GAAGTACCAGGCGGAGAGAGTGGAGAGTGGCACTGAATGGAACCGTGAAGCTT 481
54  userCysValAlaCysSerArgPheProAsnPheserIleLeuTyrrPL 71
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
480  ATCCGTGTGGCTGCTGACCGCTTCCCACTTCAGCATCTCTACTGCGC 431
71  euGlyAsnGlySerPheIleGluHisLeuProGlyArgLeuTrp.GluG1 87
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
430  TGGCAATGTTCTCTTCATGTAGCAGCTCCAGCGCCGAGCTGTGGGAGAGG 381
87  ySerThrSerArgGluArgGlySerThrGlyThrIleLeuCysLysAlaL 104
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
380  GAGCACACGCGGGAACGTGGAGACAGAGTGAACGATCTTTCAGAGGCGCT 331
104  euValLeuGluGlnLeuThrProAlaLeuHisSerThrAsnPheserCys 120
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
330  TGGTCTGAGACAGCTGACACTGCTGCCCTGCACAGCAGCACTTCCTCTGT 281
121  ValLeuValAspProGluGlnValValGlnArgHisValValLeuAlaG1 137
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
280  GTGCTCGTGGAGCCCTGAACAGAGTTGTCCAGCGTCAGTCGTCCTGGCCCA 231
137  nLeuTrpAlaGlyLeuArgAlaThrLeuProProThrGlnGluAlaLeuP 154
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
230  GCTGGGCTGGCTGAGGAGCAACTTGTCCCTCCCAAGAGAGCCCTGCGC 181
154  roSerSerHisSerSerProGlnGlnGlnGly 164
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
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seq_name: gb_est2:BF375685

seq_documentation_block:

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DEFINITION RC5-ST0300-151299-031-E04 ST0300 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF375685
VERSION BF375685.1 GI:11337710
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 515)

REFERENCE

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

TITLE

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/ICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC56t2-RC5-ST0300-151299-031-E04&t3=1999-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 44
High quality sequence stop: 60.
Location/Qualifiers

FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="ST0300"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site.1: SmaI; Site.2: SmaI; A mini-library was made by cloning products derived from ORSITES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 105 a 163 c 149 g 98 t
ORIGIN

alignment_scores:

Quality: 622.00 Length: 133
Ratio: 4.937 Gaps: 1
Percent Similarity: 94.737 Percent Identity: 92.481

alignment_block:

US-09-786-130-1 x BF375685 ..

Align seg 1/1 to: BF375685 from: 1 to: 515

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33  GlnCysProAlaLeuGluValThrTrpProGluValAluValProLeuAs 49
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2  GAGATCCAGCATTTGGAAGTGAAGTCCGCCAGAGAGGAAGTCCCACTGAA 51
49  nGlyThrLeuSerLeu.SerCysValAlaCysSerArgPheProAsnPh 65
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
52  TGGAAAGCTCAGCGTGGTGGGTGGCTGGCCAGCGCTTCCCACTTC 101
66  SerIleLeuTyrrTPLeuGlyAsnGlySerPheIleGluHisLeuProG1 82
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
102  AGCATCTCTACTGTGGCTGGCAATGTTTCCTTCATGTAGACACCTCCAGG 151
82  yArgLeuTrpGluGlySerThrSerArgGluArgGlySerThrGlyThg 99
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
152  CCGACTGTGGGAGGAGGACACAGCCGTTAAAGTGTTGGAGACAGAGGTAC 201
99  InLeuCysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSer 115
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
202  AGCTGTGCAAGGCTTGGTGGCTGGAGCAGCTACCCCTGCTGCACAGC 251
116  ThrAsnPheserCysValLeuValAspProGluGlnValValGlnArgH1 132
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
252  ACCAAGCTTTTCTGTGCTGCTGTGAGCCCTGAACAGGTGTCACAGCYCA 301
132  sValValLeuAlaGlnInLeuTrpAlaGlyLeuArgAlaThrLeuProTr 149
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302  GCTGCTCTGGGCCAGCTCTGGGCTGGGCTGTGAGGCGCAACTTGTCCCA 351
149  hrGlnGluAlaLeuProSerSerHisSerSerProGlnGlnGlnGly 164
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DEFINITION 603040310F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5181242 5',
mRNA sequence.
ACCESSION B1822872
VERSION B1822872.1 GI:15934422
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 901)
NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LAM11452 row: c column: 03
High quality sequence stop: 856.
Location/Qualifiers
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/lab_host="DH10B"
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source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: This is a NIH-MGC Library."
BASE COUNT 188 a 276 c 245 g 192 t
ORIGIN
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 Ratio: 4.252 Gaps: 7
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US-09-786-130-1 x B1822872 ..
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17 rlyAspProGlySerProSerGlnProProValPheProAlaAlaGlyGlnC 34
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483 AANAAGACCCCTGCCCTCCAGCCCCCAGCTGTCCAGCAGCTAACAGCT 532
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34 yspProAlaLeuGluValIrrTrpProGluValGluValProLeuAnGly 50
|||||
533 GTCGAGCATGGAGAGTGAAGCTGCCAGAGTGAATGCCACTGATGCA 582
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51 ThrLeuSerLeuSerCysValAlaCysSerArg.PheProAsnPheSerI 67
|||||
583 ACGTGAAGCTTATCCTGTGTGGCTGCACGCCGCTTCCCACTTACAGA 632

67 leLeuTyr.ThrLeuGluAsn.GlySerPheIleGluHisLeuProGluA 83
|||||
633 TCCCTCAAGCTGGCTGGGCAACTGTCCTTCATTTGACACCTCCAGGCC 682
|||||
83 rglLeuTrpGlu.GlySerThrSerArgGluArgGlySerThrGlyThrG 99
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683 GACTGTGGCAGCGGAGGAGCAGCCGAGACCTGGAGACAGGTGAGCCCA 732
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99 nleuCysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSer 116
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733 GCTGTGCAAGCCCTGTGGCTGGAGCAGCTGACCCCTGGCTCCAGGCA 782
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783 CCAATTTCTCTCTGTGTGCTGTGACCTTGAACAGGTTGGCCAGCTCC 832
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132 sValValIleuAlaGlnLeu...TrpAlaGluLeuArgAlaThrLeuPro 148
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seq_documentation_block:
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DEFINITION CM2-ST0284-061299-046-d12 ST0284 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW393194
VERSION AW393194.1 GI:6897853
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 538)
HCGP <http://www.ludwig.org.br/ORSTES>.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar. 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl-CM2&tl2-CM2-ST0284-061299-046-d12&tl3=1999-12-06&tl4=1>)
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High quality sequence stop: 500.
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/organism="Homo sapiens"
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/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 104 a 152 c 174 g 108 t
ORIGIN
alignment_scores:

Quality: 594.00 Length: 133
Ratio: 4.677 Gaps: 6
Percent Similarity: 95.489 Percent Identity: 94.737

alignment_block:

US-09-786-130-1 x AW393194/rev ..

Align seg 1/1 to reverse of: AW393194 from: 1 to: 538

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|||||
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54 user.CysValAlaCysSerArgPheProAsn.PheSerIleLeuTyrTr 70
|||||
481 ATCCTTGTTGGCTGCAGCGGCTTCCCAACTTTCAGCATCTCTACTG 432
|||||
70 pleuGlyAsnGlySerPheIle.GluHisLeu.ProGlyArgLeuTrpG1 86
|||||
431 GCTGGCAATGTTCTTCATTGGAGCACCTCCCGAGCGGACTGTGGGA 382
|||||
86 uGlySerThrSerArg.GluArgGlySerThrGlyThrGln.LeuCysLy 102
|||||
381 GGGAGACACCGCGGGGAACGTGGGAGACAGGTACGACGCTGTGCAA 332
|||||
102 sAlaLeuValLeuGlnLeuThrProAlaLeuHisSerThrAsnPhes 119
|||||
331 GGCCTTGCTGTGAGCAGCTGACCCCTGCCCTGCACAGCACCACTTCT 282
|||||
119 erCysValLeuValAspProGluGlnValAlaGlnArgHisValLeu 135
|||||
281 CCTGTGTGCTGTGAGACCTGAACAGGTGTGCCAGCGTCAAGTGTCTG 232
|||||
136 AlaGlnLeuThrPpaGlyLeuArgAlaThrLeuProThrGlnGlnAl 152
|||||
231 GCCAGCTGTGGGCTGGGCTGAAGGGCAACCTTGCCCCCAGCCCAAGAAGC 182
|||||
152 aLeuProSerSerHisSerSerProGlnGlnGly 164
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181 CTTGCCCTCCAGCCACAGCATCTCACAGCAGCAGAGGT 145
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 22:51:49 ; Search time 66.54 Seconds
(Without alignments)
426.378 Million cell updates/sec

Title: US-09-786-130-1
Perfect score: 870
Sequence: 1 TPVSQTTTAAATASVRSKDP.....TLPPQALPSSHSPPQOQG 164

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	870	100.0	194	4	Q9UBR7	Q9ubr7 homo sapien
3	525	60.3	161	4	Q9NZ49	Q9nza9 homo sapien
4	523.5	60.2	193	11	Q9JIN2	Q9jin2 ratius norv
5	523	60.1	191	11	Q9ZOM9	Q9zom9 mus musculu
6	515	54.9	193	11	Q9QUH2	Q9quh2 mus musculu
7	477.5	54.9	192	11	Q9ZON0	Q9zon0 mus musculu
8	302.5	34.8	99	11	Q9CY30	Q9cy30 mus musculu
9	217	24.9	218	12	Q9TMI3	Q9tmi3 molluscum c
10	205	23.6	235	12	Q98Z22	Q98z22 molluscum c
11	164	18.9	133	12	Q98Z21	Q98z21 molluscum c
12	124	14.3	161	12	Q910Q1	Q910q1 lumby skin
13	115.5	13.3	136	12	Q9DHU8	Q9dhu8 yaba-like d
14	104.5	12.0	120	12	Q57169	Q57169 vaccinia vi
15	98.5	11.3	124	12	P87608	P87608 cowpox viru
16	96.5	11.1	658	4	Q9NZN0	Q9nzn0 homo sapien

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20	94.5	10.9	126	12	Q07044	Q07044 variola vir
21	93.5	10.7	126	12	Q85357	Q85357 variola vir
22	93.5	10.7	126	12	Q89067	Q89067 variola vir
23	93	10.7	1034	5	Q9TXP2	Q9txp2 caenorhabdi
24	92.5	10.6	138	12	Q85319	Q85319 ectromella
25	92.5	10.6	354	11	Q9ER66	Q9er66 mus musculu
26	92.5	10.6	686	11	Q9ERS6	Q9ers6 mus musculu
27	84.5	9.7	286	10	Q9W022	Q9w022 arabidopsis
28	84.5	9.7	291	10	Q9ZS87	Q9zs87 arabidopsis
29	84.5	9.7	341	10	Q93YW7	Q93yw7 arabidopsis
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31	82.5	9.5	1241	4	Q60500	Q60500 homo sapien
32	82.5	9.5	2043	5	Q96943	Q96943 geodia cydo
33	82	9.4	794	2	P72249	P72249 rhodobacter
34	81	9.3	627	5	Q9XW47	Q9xw47 rhodobacter
35	81	9.3	1478	11	Q88923	Q88923 ratius norv
36	81	9.3	1487	11	Q92174	Q92174 ratius norv
37	81	9.3	1616	4	Q15054	Q15054 homo sapien
38	80	9.2	359	5	Q26596	Q26596 schistosoma
39	80	9.2	674	4	Q9NV06	Q9nv06 homo sapien
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41	79	9.1	313	8	Q9BGV2	Q9bgv2 macaca fasc
42	79	9.1	628	10	Q9XIC7	Q9xic7 arabidopsis
43	79	9.1	628	10	Q94F63	Q94f63 arabidopsis
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DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	MC51L-53L-54L HOMOLOG (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99263157; PubMed=10329540;			
RA	Xiang Y., Moss B.;			
RT	"Identification of human and mouse homologs of the MC51L-53L-54L			
RT	family of secreted glycoproteins encoded by the Molluscum contagiosum			
RT	poxvirus.";			
RL	Virology 257:297-302(1999).			
DR	EMBL: AF122908; AAD41053.1; -			
DR	InterPro: IPR003006; Ig_MHC.			
DR	Pfam: PF00047; Ig, 1.			
FT	NON_TER			
SO	SEQUENCE	184 AA;	19629 MW;	F4B12D64BA6FD3A2 CRC64;

Query Match Best Local Similarity 100.0%; Score 870; DB 4; Length 184; Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TPVSQTTTAAATASVRSKDPSPVPVPAKQCPALEVTWPEVEVPLNGTSLSCVACS	60
DB	21	TPVSQTTTAAATASVRSKDPSPVPVPAKQCPALEVTWPEVEVPLNGTSLSCVACS	80
QY	61	REPNSITLYWNGSFTLHLPGRIMEGSTSRERSTGTQLCKALVLEDTTALHSTNSC	120
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RP SEQUENCE FROM N.A.

RT "Interleukin-18 binding protein: a novel modulator of the Th1 cytok;
RT response.";

Query Match	54.9%	Score 477.5	DB 11	Length 192
Best Local Similarity	68.3%	Pred. No. 4.6e-42		
Matches 95	Conservative 10	Mismatches 31	Indels 3	Gaps 2

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		PRT;
		99 AA

RN [1]
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RC STRAIN=C57BL/6J; TISSUE=TONGUE;

RC STRAIN=CS7BL/6J; TISSUE=NONUNE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hata A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanae I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glasi C., Ring B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikdel I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
RA Blake J., Borfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Nordone P., Ring B., Ringwald L., Wiedmaier I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Borris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
EMBL: AK009877; BAB26558.1; -
DR MGD: MGI:1333800; Igfbp.
FT NON_TER 1 1
SQ SEQUENCE 99 AA: 10869 MW: 2CB08739D5DABE8C CRC64;

Query Match	34.88;	Score 302.5;	DB 11;	Length 99;
Best Local Similarity	67.48;	Pred. No. 4e-24;		

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		218 AA

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RT	J. Gen. Virol.	81:1323-1230(2000).
RT	18 binding proteins. "	
RT	Ectromedulla, vaccinia and cowpox viruses encode secreted interleukin	
RA	Smith V. P., Bryant N.A., Alcamal A.;	
RA	MEDLINE-20231932; PubMed-10769064;	
RC	STRAIN-MADRID 99;	
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OC	NCBI_TaxID=10280;	
OX	NCBI_TaxID=10280;	
RN	SPROUCE FROM N.A.	
RP	SPROUCE FROM N.A.	
GN	054L.	
OS	Molluscum contagiosum virus subtype 1 (MCV1).	
OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
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OX	NCBI_TaxID=10280;	
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GN	054L.	
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OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC	NCBI_TaxID=10280;	
OX	NCBI_TaxID=10280;	
RN	SPROUCE FROM N.A.	
RP	SPROUCE FROM N.A.	
GN	054L.	
OS	Molluscum contagiosum virus subtype 1 (MCV1).	
OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC	NCBI_TaxID=10280;	
OX	NCBI_TaxID=10280;	
RN	SPROUCE FROM N.A.	
RP	SPROUCE FROM N.A.	
GN	054L.	
OS	Molluscum contagiosum virus subtype 1 (MCV1).	
OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC	NCBI_TaxID=10280;	
OX	NCBI_TaxID=10280;	
RN	SPROUCE FROM N.A.	
RP	SPROUCE FROM N.A.	
GN	054L.	
OS	Molluscum contagiosum virus subtype 1 (MCV1).	
OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC	NCBI_TaxID=10280;	
OX	NCBI_TaxID=10280;	
RN	SPROUCE FROM N.A.	
RP	SPROUCE FROM N.A.	
GN	054L.	
OS	Molluscum contagiosum virus subtype 1 (MCV1).	
OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC	NCBI_TaxID=10280;	
OX	NCBI_TaxID=10280;	
RN	SPROUCE FROM N.A.	
RP	SPROUCE FROM N.A.	
GN	054L.	
OS	Molluscum contagiosum virus subtype 1 (MCV1).	
OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC	NCBI_TaxID=10280;	
OX	NCBI_TaxID=10280;	
RN	SPROUCE FROM N.A.	
RP	SPROUCE FROM N.A.	
GN	054L.	
OS	Molluscum contagiosum virus subtype 1 (MCV1).	
OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC	NCBI_TaxID=10280;	
OX	NCBI_TaxID=10280;	
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RP	SPROUCE FROM N.A.	
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OS	Molluscum contagiosum virus subtype 1 (MCV1).	
OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC	NCBI_TaxID=10280;	
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RN	SPROUCE FROM N.A.	
RP	SPROUCE FROM N.A.	
GN	054L.	
OS	Molluscum contagiosum virus subtype 1 (MCV1).	
OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC	NCBI_TaxID=10280;	
OX	NCBI_TaxID=10280;	
RN	SPROUCE FROM N.A.	
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OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
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OX	NCBI_TaxID=10280;	
RN	SPROUCE FROM N.A.	
RP	SPROUCE FROM N.A.	
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OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC	NCBI_TaxID=10280;	
OX	NCBI_TaxID=10280;	
RN	SPROUCE FROM N.A.	
RP	SPROUCE FROM N.A.	
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OS	Molluscum contagiosum virus subtype 1 (MCV1).	
OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC	NCBI_TaxID=10280;	
OX	NCBI_TaxID=10280;	
RN	SPROUCE FROM N.A.	
RP	SPROUCE FROM N.A.	
GN	054L.	
OS	Molluscum contagiosum virus subtype 1 (MCV1).	
OC	VIRUSES; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC	NCBI_TaxID=10280;	
OX	NCBI_TaxID=10280;	
RN	SPROUCE FROM N.A.	
RP	SPROUCE FROM N.A.	
GN	054L.	
OS	Molluscum contagiosum virus subtype 1 (MCV1).	

Query Match	24.9%	Score 217;	DB 12;	Length 218;
Best Local Similarity	-39.9%	Pred. No. 8.3e-15;		
Matches 55; Conservative	24;	Mismatches 45;	Indels 14;	Gaps 6;

[illegible]

RESULT	ID	PRELIMINARY;	PRT;	235 AA.
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DT	01-FEB-1997 (TrEMBLrel. 02, Last sequence update)			
DT	01-NOV-1998 (TrEMBLrel. 08, Last annotation update)			
DE	MC054L.			
GN	MC054L.			
OS	Molluscum contagiosum virus subtype 1 (MCV1).			
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;			
OC	Molluscipoxvirus.			
OX	NCBI_TaxID=10280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96325459; PubMed=8670425;			
RA	Senkovich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,			
RA	Moss B.;			
RT	"Genome sequence of a human tumorigenic poxvirus: Prediction of			
RT	specific host response-evasion genes.";			

1B	Q910Q1	PRELIMINARY;	161 AA.
1C	Q910Q1	PRT;	

RA Lee H.J.;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 19, 2002, 21:48:54 ; Search time 57.81 Seconds
(without alignments)
315.103 Million cell updates/sec

Title: US-09-786-130-1
Perfect score: 870
Sequence: 1 TPVSGTTTAATATVSRFTKDP.....TLPPTEALPSHSSEPPQOG 164

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A.Geneseq_032802:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
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19: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	870	100.0	164	21	AAV83951	Human mature inter-
2	870	100.0	192	20	AAW98004	Human interleukin-
3	870	100.0	194	21	AAV96292	Human IGFAW-4 immu
4	870	100.0	194	21	AAV83985	Full length human
5	742	85.3	197	20	AAW98006	Human interleukin-
6	727	83.6	137	21	AAV83982	Human IL-18 bindin
7	525	60.3	161	20	AAW98007	Human interleukin-
8	515	59.2	165	21	AAV83952	Mouse mature inter
9	515	59.2	193	21	AAV83989	Full length mouse
10	441	50.7	117	21	AAV83986	Mouse IL-18 bindin
11	257	29.5	113	20	AAW98005	Human interleukin-

12	244	28.0	47	21	AAV83964	Human IL-18 bindin
13	209	24.0	40	20	AAW98008	Human interleukin-
14	122	14.0	55	20	AAV12716	Human 5' EST seque
15	114	13.1	29	21	AAV83960	Human interleukin
16	114	13.1	55	20	AAV12556	Human 5' EST seque
17	106	12.2	134	18	AAW26423	Swinepox virus H1n
18	106	12.2	14	22	AAW68244	Protein encoded by
19	102.5	11.8	45	21	AAV83968	Mouse IL-18 bindin
20	101	11.6	23	21	AAV83958	Human interleukin
21	96.5	11.1	59	20	AAV14130	Human IL-18D prote
22	96.5	11.1	658	20	AAV22164	Human TIGIR prote
23	96.5	11.1	686	20	AAV14128	Human IL-18D prot
24	93.5	10.7	2134	22	AAV27624	Human human diagno
25	92.5	10.6	385	22	ABG02770	Novel human diagno
26	92.5	10.6	532	22	ABG20407	Novel human diagno
27	92.5	10.6	717	22	ABG24052	Novel human diagno
28	92.5	10.6	744	22	ABG02772	Novel human diagno
29	90	10.3	49	21	AAV83983	Human IL-18 bindin
30	88.5	10.2	766	22	ABG14630	Novel human diagno
31	87.5	10.1	949	22	ABG06446	Novel human diagno
32	84.5	9.7	341	21	AAV41565	Arabidopsis thalia
33	82.5	9.5	1241	20	AAV42167	Human nephrit prol
34	82.5	9.5	1241	22	AAV47047	Human nephrit. Ho
35	81	9.3	430	22	ABG14501	Novel human diagno
36	81	9.3	945	20	AAV06119	Human C17A intera
37	80	9.2	22	21	AAV83953	Human interleukin
38	80	9.2	674	22	AAV82888	Human protein sequ
39	80	9.2	1072	22	ABG04157	Novel human diagno
40	79.5	9.1	307	22	AAV40911	Protonibacterium
41	79	9.1	237	20	AAV6187	Human bladder tumo
42	79	9.1	467	21	AAV30869	Arabidopsis thalia
43	79	9.1	598	21	AAV30868	Arabidopsis thalia
44	79	9.1	628	21	AAV30867	Arabidopsis thalia
45	79	9.1	674	20	AAV99891	Human growth regul

ALIGNMENTS

RESULT 1
AAV83951 standard; Protein; 164 AA.
XX
AC AAV83951;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human mature Interleukin 18 binding protein.
XX
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease.
XX
OS Homo sapiens.
XX
PN WO200012555-A1.
XX
PD 09-MAR-2000.
XX
PF 18-NOV-1998; 98WO-9P05186.
XX
PR 01-SEP-1998; 98JP-0247588.
PR 18-NOV-1998; 98JP-0327914.
(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
Torioe K, Tanial M, Kurimoto M,
WPI: 2000-237850/20.
DR N-PSDB; AAA11002.
XX
DR Interleukin 18-binding protein with activity of regulating
XX physiological actions of interleukin 18, useful as regulator and drug
PT

PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction -
PS Claim 1; Page 44-45; 71pp; Japanese.
XX
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the mature
CC human interleukin 12 binding protein.
XX
SQ Sequence 164 AA;
Query Match 100.0%; Score 870; DB 21; Length 164;
Best Local Similarity 100.0%; Pred. No. 1.2e-78;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPVSQTTTAATASVSTKDCPSQPPVFPAAKQCPALVETWPEVPLNGTSLSCVACS 60
DB 1 TPVSQTTAATASVSTKDCPSQPPVFPAAKQCPALVETWPEVPLNGTSLSCVACS 60
QY 61 RPPNFSIIYWGNGSFIEHLPGRLEWEGSTSRERGSTGTOLKALVLEDTLPALHSTNFS 120
DB 61 RPPNFSIIYWGNGSFIEHLPGRLEWEGSTSRERGSTGTOLKALVLEDTLPALHSTNFS 120
QY 121 VLVDPEQVYVORHVVLAQLMAGLRATLPPTQEALPSSHSSPQOQG 164
DB 121 VLVDPEQVYVGRHVLAQLMAGLRATLPPTQEALPSSHSSPQOQG 164
DB 121 VLVDPEQVYVGRHVLAQLMAGLRATLPPTQEALPSSHSSPQOQG 164
RESULT 2
AAW98004
ID AAW98004 standard; Protein: 192 AA.
XX
AC AAW98004;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human interleukin-18 binding protein splice variant IL-18Bpa.
XX
KW Interleukin-18 binding protein; IL-18BP; IL-18Bpa; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
KW ischemic heart disease; ischemic brain injury; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..192
FT /note= "mature protein"
XX
PN WO9909063-A1.
PD 25-FEB-1999.
XX
PE 13-AUG-1998; 98WO-IL00379.
XX
XX 22-JUL-1998; 98IL-0125463.
PR 14-AUG-1997; 97IL-0121554.
PR 27-AUG-1997; 97IL-0121639.
PR 29-SEP-1997; 97IL-0121860.
PR 06-NOV-1997; 97IL-0122134.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
PI Dinarello C, Kim SH, Novick D, Rubinstein M;
XX
DR WPI; 1999-180975/15.

DR N-PSDB: AAX24749.
XX
XX New interleukin-18 binding protein - useful for treating human
PT diseases, including autoimmune disease and inflammation
PS Claim 3; Page 53-54; 100pp; English.
XX
XX The present sequence represents a human interleukin-18 binding
CC protein (IL-18BP) splice variant designated IL-18Bpa. This
CC is one of 4 novel splice variants (see also AAW98005-07), all
CC putative soluble proteins, encoded by cDNA clones (see AAX24749-52)
CC detected following a screening of human peripheral blood monocyte,
CC Jurkat T-cell, peripheral blood mononuclear cell and spleen cell
CC cDNA libraries. IL-18Bpa is the most abundant of the 4 splice
CC variants and is a putative member of the immunoglobulin superfamily.
CC Its first 40 residues perfectly match the N-terminal sequence of
CC urinary IL-18BP (see AAW98008). IL-18BP polypeptides capable of
CC binding IL-18 and/or modulating and/or blocking IL-18 activity are
CC provided. Methods for their isolation and recombinant production,
CC DNA vectors expressing them, vectors useful for their expression in
CC humans and other mammals, and antibodies against them are also
CC provided. IL-18BP polypeptides, and DNA encoding them, can be used
CC to treat conditions requiring the protein (claimed). Conditions
CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,
CC graft rejections, inflammatory bowel disease, sepsis, multiple
CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic
CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
CC also useful for purifying IL-18 (claimed).
XX
SQ Sequence 192 AA;
Query Match 100.0%; Score 870; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-78;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPVSQTTTAATASVSTKDCPSQPPVFPAAKQCPALVETWPEVPLNGTSLSCVACS 60
DB 29 TPVSQTTAATASVSTKDCPSQPPVFPAAKQCPALVETWPEVPLNGTSLSCVACS 88
QY 61 RPPNFSIIYWGNGSFIEHLPGRLEWEGSTSRERGSTGTOLKALVLEDTLPALHSTNFS 120
DB 89 RPPNFSIIYWGNGSFIEHLPGRLEWEGSTSRERGSTGTOLKALVLEDTLPALHSTNFS 148
QY 121 VLVDPEQVYVORHVVLAQLMAGLRATLPPTQEALPSSHSSPQOQG 164
DB 149 VLVDPEQVYVGRHVLAQLMAGLRATLPPTQEALPSSHSSPQOQG 192
RESULT 3
AAW96292
ID AAW96292 standard; protein: 194 AA.
XX
AC AAW96292;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human IGFAM-4 immunoglobulin.
XX
KW Human; immunoglobulin; IGFAM-4; IGFAM; immune disorder; cancer;
KW infection; inflammation; haematopoiesis; AIDS; allergy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= signal_peptide
FT Protein 31..194
FT /label= IGFAM-4
XX
PN WO200029583-A2.
PD 25-MAY-2000.

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XX 19-NOV-1999; 99WO-US27566.
PF
XX 19-NOV-1998; 99US-0113635.
PR 22-DEC-1998; 98US-0113635.
PR 07-APR-1999; 99US-0128194.
XX
PA (INCYTE) INCYTE PHARM INC.
XX
PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR,
PI Lu DM, Lai P, Hillman JL, Yang J;
XX
DR WPI; 2000-387796/33.
DR N-PSDB; AAA27384.
XX
PT Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT protein is useful for preventing and treating disorders associated with
PT altered levels of the protein such as cancer, immune system disorders
PT
XX
PS Claim 1; Page 81; 105pp; English.
XX
CC The present sequence is the human immunoglobulin superfamily protein
CC IGFAM-4. Its gene was isolated from a cDNA library of prostate tumour
CC tissue. It is expressed in nervous, haematopoietic and immune and
CC cardiovascular tissue, where cancer and inflammation are common. The
CC gene, protein, its antibodies, agonists and antagonists are suitable for
CC diagnosing and treating many diseases, including cancer, immune system
CC disorders (such as inflammation, AIDS, allergies, anaemia,
CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC systemic lupus erythematosus and ulcerative colitis), complications of
CC cancer, haemodialysis and extracorporeal circulation, trauma and
CC haematopoietic cancer (such as leukaemia) and infections caused by
CC bacteria, viruses, fungi or parasites.
XX
SQ Sequence 194 AA;

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Query Match 100.0%; Score 870; DB 21; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.5e-78;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TPVSQTTTAAATASVRSKDCPSOPVFPAAKOCPALEVTWPEVEVPLNGTSLSCVACS 60
DB 31 tpvsqtttaataasvrskdcpsqpvfpaaqgcpalvewpevevplngtislscvacs 90
QY 61 RFPNFSILYWLGNCSFTIEHLPGRLMEGSTSRERGSTGTQLCKALVLEBOLTPALHSTNFS 120
DB 91 rfpnfssilywlgnsgfiehlpgrlwegstsrergstgtqlckalvleqplpalhstnfsc 150
QY 121 VLVDPQGVQRRHVYLAOLMAGLRATLPPTQEPALPSSHSSPOQOG 164
DB 151 vlvdpqgvqrrhvvlaqlwaglratlpttqepalpsshspsqgqg 194

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RESULT 4
AAW83985
ID AAY83985 standard; Protein; 194 AA.
AC AAY83985;
XX
DT 28-JUL-2000 (first entry)
XX
DE Full length human interleukin 18 binding protein.
XX
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease.
XX
OS Homo sapiens.
XX

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FH Key Location/Qualifiers
FT Peptide 1..30
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FT Protein 31..194
FT /label= "mature human IL-18 binding protein"
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PD 09-MAR-2000.
XX
PE 18-NOV-1998; 98WO-JP05186.
XX
PR 01-SEP-1998; 98JP-0247588.
PR 18-NOV-1998; 98JP-0327914.
XX
PA (HAYASHIBARA SEIBUTSU KAKAKU.
XX
PI Torigoe K, Tanai M, Kurimoto M;
XX
DR WPI; 2000-237850/20.
DR N-PSDB; AAA11007.
XX
PT Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction
XX
PS Example 2; Page 63-64; 71pp; Japanese.
XX
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the full
CC length human interleukin 12 binding protein.
XX
SQ Sequence 194 AA;

```

```

Query Match 100.0%; Score 870; DB 21; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.5e-78;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TPVSQTTTAAATASVRSKDCPSOPVFPAAKOCPALEVTWPEVEVPLNGTSLSCVACS 60
DB 31 tpvsqtttaataasvrskdcpsqpvfpaaqgcpalvewpevevplngtislscvacs 90
QY 61 RFPNFSILYWLGNCSFTIEHLPGRLMEGSTSRERGSTGTQLCKALVLEBOLTPALHSTNFS 120
DB 91 rfpnfssilywlgnsgfiehlpgrlwegstsrergstgtqlckalvleqplpalhstnfsc 150
QY 121 VLVDPQGVQRRHVYLAOLMAGLRATLPPTQEPALPSSHSSPOQOG 164
DB 151 vlvdpqgvqrrhvvlaqlwaglratlpttqepalpsshspsqgqg 194

```

```

RESULT 5
AAW98006
ID AAW98006 standard; Protein; 197 AA.
AC AAW98006;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human interleukin-18 binding protein splice variant IL-18Bpc.
XX
KW Interleukin-18 binding protein; IL-18BP; IL-18Bpc; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
KW ischemic heart disease; ischemic brain injury; therapy.
XX
OS Homo sapiens.
XX

```

```
XX Key Location/Qualifiers
FH Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..197
FT /note= "mature protein"
XX
XX WO9909063-A1.
XX
XX 25-FEB-1999.
XX
XX 13-AUG-1998; 98WO-IL00379.
XX
XX 22-JUL-1998; 98IL-0125463.
XX 14-AUG-1997; 97IL-0121554.
XX 27-AUG-1997; 97IL-0121639.
XX 29-SEP-1997; 97IL-0121860.
XX 06-NOV-1997; 97IL-0122134.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Dinarello C, Kim SH, Novick D, Rubinstein M;
XX WPI: 1999-180975/15.
XX N-PSDB: AAX24751.
XX
XX New interleukin-18 binding protein - useful for treating human
XX diseases, including autoimmune disease and inflammation
XX
XX Claim 3; Page 58-59; 100pp; English.
XX
XX The present sequence represents a human interleukin-18 binding
XX protein (IL-18BP) splice variant designated IL-18BPC. This is one
XX four novel splice variants (see also AAW98004-07), all putative
XX soluble proteins, that are encoded by cDNA clones (see AAX24749-52)
XX detected following a screening of human peripheral blood monocyte,
XX Jurkat T-cell, peripheral blood mononuclear cell and spleen cell
XX cDNA libraries. IL-18BPC is a low abundance variant. IL-18BP
XX polypeptides capable of binding IL-18 and/or modulating and/or
XX blocking IL-18 activity are provided, as are methods for their
XX isolation and recombinant production, DNA vectors expressing them,
XX vectors useful for their expression in humans and other mammals,
XX and antibodies against them. IL-18BP polypeptides, and DNA encoding
XX them, can be used to treat conditions requiring the protein
XX (claimed). Conditions include autoimmune diseases, type I diabetes,
XX rheumatoid arthritis, graft rejections, inflammatory bowel disease,
XX sepsis, multiple sclerosis, ischemic heart diseases, ischemic brain
XX injury, chronic hepatitis, psoriasis, and chronic/acute
XX pancreatitis. IL-18BP is also useful for purifying IL-18 (claimed).
XX
XX Sequence 197 AA;
XX
XX Query Match 85.3%; Score 742; DB 20; Length 197;
XX Best Local Similarity 100.0%; Pred. No. 8.2e-66;
XX Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TPVSOTTTAATASVSTKDCPSOPVFPAAKQCPALAEVTPVEVPLNGTSLSCVACS 60
XX |||||||
XX Db 29 tpvsqttaatasvstkdpcpsppvfpaakqcpalevtpevevplngtislscvacs 88
XX
XX 61 RFPNFSILYWGNGSFIEHLPGRLWEGSTSRBRGSGTQCLKALVLEOLTPALHSTNFS 120
XX |||||||
XX Db 89 rfpnfsilywngngsfiehlpgrlwegstsrbrgstgtqlckalvleqltpalhstntsc 148
XX
XX 121 VLVDPEQVYVQRHVLAQL 139
XX |||||||
XX Db 149 vlvdpeqvvyqrhvvlaqlw 167
XX
XX RESULT 6
XX ID AAW83982 standard; Protein: 137 AA.
```

```
XX AAW83982;
XX
XX 28-JUL-2000 (first entry)
XX
XX Human IL-18 binding protein 5' RACE fragment #1 encoded protein.
XX
XX Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
XX regulator; drug; sensitivity disease; organ rejection; organ transplant;
XX autoimmune disease; rapid amplification of cDNA ends; RACE.
XX
XX Homo sapiens.
XX
XX WO200012555-A1.
XX
XX 09-MAR-2000.
XX
XX 18-NOV-1998; 98WO-JP05186.
XX
XX 01-SEP-1998; 98JP-0247588.
XX 18-NOV-1998; 98JP-0327914.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Toriigoe K, Taniai M, Kurimoto M;
XX WPI: 2000-237850/20.
XX N-PSDB: AAL11004.
XX
XX Interleukin 18-binding protein with activity of regulating
XX physiological actions of interleukin 18, useful as regulator and drug
XX for sensitivity diseases and organ rejection and in treating diseases
XX due to excess immune reaction -
XX
XX Example 2; Page 60-61; 71pp; Japanese.
XX
XX The invention relates to novel interleukin 18 (IL-18)-binding proteins
XX from humans or mice which act as regulators and drugs for sensitivity
XX diseases and organ rejection and in treating diseases due to excess
XX immune reaction, e.g. in slowing down rejection after organ transplant,
XX and in treating autoimmune diseases. This sequence represents the
XX protein encoded by the initial fragment isolated by a 5' RACE (Rapid
XX Amplification of cDNA Ends) reaction for the 5' end of the interleukin
XX 12 binding protein coding sequence.
XX
XX Sequence 137 AA;
XX
XX Query Match 83.6%; Score 727; DB 21; Length 137;
XX Best Local Similarity 100.0%; Pred. No. 1.0e-64;
XX Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TPVSOTTTAATASVSTKDCPSOPVFPAAKQCPALAEVTPVEVPLNGTSLSCVACS 60
XX |||||||
XX Db 1 tpvsqttaatasvstkdpcpsppvfpaakqcpalevtpevevplngtislscvacs 60
XX
XX 61 RFPNFSILYWGNGSFIEHLPGRLWEGSTSRBRGSGTQCLKALVLEOLTPALHSTNFS 120
XX |||||||
XX Db 61 rfpnfsilywngngsfiehlpgrlwegstsrbrgstgtqlckalvleqltpalhstntsc 120
XX
XX 121 VLVDPEQVYVQRHVLAQL 137
XX |||||||
XX Db 121 vlvdpeqvvyqrhvvlaql 137
XX
XX RESULT 7
XX ID AAW98007 standard; Protein: 161 AA.
XX
XX AAW98007;
XX
XX 21-JUN-1999 (first entry)
XX
```

XX		Human interleukin-18 binding protein splice variant IL-18BPd.
XX	KM	Interleukin-18 binding protein; IL-18BP; IL-18Bpd; splice variant;
XX	KM	human; autoimmune disease; inflammation; diabetes; pancreatitis;
XX	KW	rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
XX	KW	psoriasis; inflammatory bowel disease; multiple sclerosis;
XX	KW	ischemic heart disease; ischemic brain injury; therapy.
OS	XX	Homo sapiens.
XX	XX	
FH	Key	Location/Qualifiers
FT	Peptide	1..28
FT	Protein	/note= "signal peptide"
FT		29..161
XX		/note= "mature protein"
PN	MO90909063-A1.	
XX		
PD	25-FEB-1999.	
XX		
PF	13-AUG-1998;	98WO-IL00379.
XX		
PR	22-JUL-1998;	98IL-0125463.
PR	14-AUG-1997;	97IL-0121554.
PR	27-AUG-1997;	97IL-0121639.
PR	29-SEP-1997;	97IL-0121860.
PR	06-NOV-1997;	97IL-0122134.
PA	(YEDA) YEDA RES & DEV CO LTD.	
PI	Dinarelllo C, Kim SH, Novick D, Rubinstein M;	
XX		
DR	WPI: 1999-1800975/15.	
DR	N-PsDB: AAX24752.	
XX		
PT	New interleukin-18 binding protein - useful for treating human	
PT	diseases, including autoimmune disease and inflammation	
XX		
PS	Claim 3; Page 60; 100pp; English.	
XX		
CC	The present sequence represents a human interleukin-18 binding	
CC	protein (IL-18BP) splice variant designated IL-18Bpd. This is one	
CC	four novel splice variants (see also AAG98004-07), all putative	
CC	soluble proteins, that are encoded by cDNA clones (see AAX24749-52)	
CC	detected following a screening of human peripheral blood monocyte,	
CC	Jurkat T-cell, peripheral blood mononuclear cell and spleen cell	
CC	cDNA libraries. IL-18Bpd is a low abundance variant. IL-18BP	
CC	polypeptides capable of binding IL-18 and/or modulating and/or	
CC	blocking IL-18 activity are provided, as are methods for their	
CC	isolation and recombinant production, DNA vectors expressing them,	
CC	vectors useful for their expression in humans and other mammals,	
CC	and antibodies against them. IL-18BP polypeptides, and DNA encoding	
CC	them, can be used to treat conditions requiring the protein	
CC	(claimed). Conditions include autoimmune diseases, type I diabetes,	
CC	rheumatoid arthritis, graft rejections, inflammatory bowel disease,	
CC	sepsis, multiple sclerosis, ischemic heart diseases, ischemic brain	
CC	injury, chronic hepatitis, psoriasis, and chronic/acute	
CC	pancreatitis. IL-18BP is also useful for purifying IL-18 (claimed).	
XX		
SQ	Sequence 161 AA;	
	Query Match 60.3%; Score 525; DB 20; Length 161;	
	Best Local Similarity 100.0%; Pred. No. 2,4e-44;	
	Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 TPVSCTTAATASVRSTDPDPCSPVPFPAKQCFALEYMEVEVPLNGTISLSCVACS 60	
Db	29 tpvsqtltaasvstkdpcspgvpfpaakqpalevtwpevypngtislscvacs 88	
OY	61 RPPNFSIIYWGNSFEHLPGRLMEGSTRRGSTG 97	
Db	89 rtpnfsiiywgnsfehlpgrihwegstrergstg 125	

[illegible]

XX	28-JUL-2000	(first entry)
DT		
XX		
DE	Full length mouse interleukin 18 binding protein.	
XX		
KW	Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;	
KM	regulator; drug; sensitivity disease; organ rejection; organ transplant;	
KX	autoimmune disease.	
XX		
OS	Mus musculus.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..28
FT	Protein	/label= signal_peptide
FT		29..193
FT		/label= "mature IL-18 binding protein"
XX		
PN	WO200012555-A1.	
PD		
XX	09-MAR-2000.	
PE		
XX	18-NOV-1998;	98WO-JP05186.
PR	01-SEP-1998;	98JP-0247588.
PR	18-NOV-1998;	98JP-0327914.
XX		
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.	
PI	Torigoe K, Tanial M, Kurimoto M;	
XX		
DR	WPI: 2000-237850/20.	
DR	N-PSDB: AAA11011.	
XX		
PT	Interleukin 18-binding protein with activity of regulating	
PT	physiological actions of interleukin 18, useful as regulator and drug	
PT	for sensitivity diseases and organ rejection and in treating diseases	
PT	due to excess immune reaction	
XX		
PS	Example 4; Page 67-69; 71pp; Japanese.	
XX		
CC	The invention relates to novel interleukin 18 (IL-18)-binding proteins	
CC	from humans or mice which act as regulators and drugs for sensitivity	
CC	diseases and organ rejection and in treating diseases due to excess	
CC	immune reaction, e.g. in slowing down rejection after organ transplant,	
CC	and in treating autoimmune diseases. This sequence represents the full	
CC	length mouse interleukin 12 binding protein.	
XX		
SO	Sequence 193 AA;	
	Query Match 59.2%; Score 515; DB 21; Length 193;	
	Best Local Similarity 66.5%; Pred. No. 2.9e-43;	
	Matches 105; Conservative 12; Mismatches 37; Indels 4; Gaps 3	
OY	1 TPVSOTTWAAATSVRSTKPCPCSPDPVFPAAKCCPALEVTWPEVEYPLNGTISLSCVACS 60	
Db	29 tsapqtl-atvltgskscpcsswspavp-tkypaldvipekeyplngltlslstaacs 85	
OY	61 RFPNFSILYWLNGSFIEHLPGRLWEGSTSRERGSTGLOCAKALVLEQLTPALHSTNFGC 120	
Db	86 rfpysillywlngsfiehlpgrlwsgstsrerhstslwlrhalvleelsplrtstnfsc 145	
OY	121 VLVDPEQVVRHVVLAQLMAGLRATLPRQGLAPSSHS 158	
Db	146 lfvdpqvaqynlllaqlwdgikltaapsqetl-shs 182	
	RESULT 10	
ID	AA83986	
XX	AA83986 standard; Protein; 117 AA.	
AC	AA83986;	
XX		

DT		28-JUL-2000	(first entry)	
XX				
DE	Mouse IL-18 binding protein 5' RACE fragment #1 encoded protein.			
XX				
KW	Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;			
KM	regulator; drug; sensitivity disease; organ rejection; organ transplant;			
XN	autoimmune disease; rapid amplification of cDNA ends; RACE.			
OS	Mus musculus.			
PN	WO200012555-A1.			
PD	09-MAR-2000.			
PJ	18-NOV-1998; 98WO-JP05186.			
PR	01-SEP-1998; 98JP-0247588.			
PS	18-NOV-1998; 98JP-0327914.			
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.			
PI	Torigoe K, Taniai M, Kurimoto M;			
DZ	WPt: 2000--237850/20.			
N-PSDB:	AAAI1008.			
PT	Interleukin 18-binding protein with activity of regulating physiological actions of interleukin 18, useful as regulator and drug for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction -			
XX				
PS	Example 4; Page 65; 71pp; Japanese.			
CC	The invention relates to novel interleukin 18 (IL-18)-binding proteins from humans or mice which act as regulators and drugs for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction, e.g., in slowing down rejection after organ transplant,			
CC	and in treating autoimmune diseases. This sequence represents the protein encoded by the initial fragment isolated by a 5' RACE (Rapid Amplification of cDNA Ends) reaction for the 5' end of the mouse interleukin 12 binding protein coding sequence.			
SQ	Sequence 117 AA;			
Query Match	50.7%; Score 441; DB 21; Length 117;			
Best Local Similarity	74.1%; Pred. No. 3.5e-36;			
Matches	83; Conservative 10; Mismatches 19; Indels 0; Gaps 0			
OY	32 KCPCPLLEVMPVEPVENLTSLISCACGSRFPPESTLYLWGSGFTEHLPGRLMEGSTSR 91 : : : : : : : : : : : : : : : : : : : Db 5 kyppladtwpkvpevlngcltlscacsrfpfysillylgnstienhprikgehtsr 64			
OY	92 ERKSGTGOLCKALVLQGLTLPALHSTNFSCVLVDPEEQVVORHVLAQLMAGLR 143 : : : : : : : : : : : : : : : : : : : Db 65 ehnrnstwlhralvalvealsplrtnsfcsclfvdpgqvgayghlllaqlwdglik 116			
RESULT	11			
ID	AAW98005			
XX	AAW98005 standard; Protein; 113 AA.			
AC	AAW98005;			
DT	21-JUN-1999 (first entry)			
DE	Human interleukin-18 binding protein splice variant IL-18BP.			
KW	interleukin-18 binding protein; IL-18BP; IL-18PBp; splice variant;			
KM	human; autoimmune disease; inflammation; diabetes; pancreatitis;			
KX	rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;			
KW	pneumonia; inflammatory bowel disease; multiple sclerosis;			
KW	ischemic heart disease; ischemic brain injury; therapy.			

```
XX OS Homo sapiens.
XX FH Key
XX FT Peptide
XX FT Protein
XX FT /note="signal peptide"
XX FT /note="mature protein"
XX PN MO9909063-A1.
XX PD 25-FEB-1999.
XX PF 13-AUG-1998; 98WO-IL00379.
XX PR 22-JUL-1998; 98IL-0125463.
XX PR 14-AUG-1997; 97IL-0121554.
XX PR 27-AUG-1997; 97IL-0121639.
XX PR 29-SEP-1997; 97IL-0121860.
XX PR 06-NOV-1997; 97IL-0122134.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI Dinarello C, Kim SH, Novick D, Rubinstein M;
XX DR WPI: 1999-180975/15.
XX DR N-PSDB; AAX24750.
XX PT New interleukin-18 binding protein - useful for treating human
XX PS diseases, including autoimmune disease and inflammation
XX PS Claim 3; Page 55; 100pp; English.
XX CC The present sequence represents a human interleukin-18 binding
XX CC protein (IL-18BP) splice variant designated IL-18Bpd. This is one
XX CC four novel splice variants (see also AAW98004-07), all putative
XX CC soluble proteins, that are encoded by cDNA clones (see AAX24749-52)
XX CC detected following a screening of human peripheral blood monocyte,
XX CC Jurkat T-cell, peripheral blood mononuclear cell and spleen cell
XX CC cDNA libraries. IL-18Bpd is a low abundance variant. IL-18BP
XX CC polypeptides capable of binding IL-18 and/or modulating and/or
XX CC blocking IL-18 activity are provided, as are methods for their
XX CC isolation and recombinant production, DNA vectors expressing them,
XX CC vectors useful for their expression in humans and other mammals,
XX CC and antibodies against them. IL-18BP polypeptides, and DNA encoding
XX CC them, can be used to treat conditions requiring the protein
XX CC (claimed). Conditions include autoimmune diseases, type I diabetes,
XX CC rheumatoid arthritis, graft rejections, inflammatory bowel disease,
XX CC sepsis, multiple sclerosis, ischemic heart diseases, ischemic brain
XX CC injury, chronic hepatitis, psoriasis, and chronic/acute
XX CC pancreatitis. IL-18BP is also useful for purifying IL-18 (claimed).
XX SQ Sequence 113 AA;

Query Match 29.5%; Score 257; DB 20; Length 113;
Best Local Similarity 98.0%; Pred. No. 6.5e-18;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPVSQTTTATASVSRSTKDCPSQPPVFPAAKQCPALEVTWPEVEVPLN 49
DB 29 tpvsqttatatsvstkdpcpsqpvpvfpakqcpalevtwpevevpls 77

RESULT 12
AAV83984
ID AAV83984 standard; Protein; 47 AA.
XX
XX AAV83984;
AC
XX
XX
DT 28-JUL-2000 (first entry)
XX
XX Human IL-18 binding protein C-terminus.
DE
```

```
XX OS Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
XX KM regulator; drug; sensitivity disease; organ rejection; organ transplant;
XX KM autoimmune disease; rapid amplification of cDNA ends; RACE.
XX OS Homo sapiens.
XX PN WO200012555-A1.
XX PD 09-MAR-2000.
XX PF 18-NOV-1998; 98WO-JP05186.
XX PR 01-SEP-1998; 98JP-0247588.
XX PR 18-NOV-1998; 98JP-0327914.
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX PI Torigoe K, Tanial M, Kurimoto M;
XX DR WPI: 2000-237850/20.
XX DR N-PSDB; AAA11006.
XX PT Interleukin 18-binding protein with activity of regulating
XX PT physiological actions of interleukin 18, useful as regulator and drug
XX PT for sensitivity diseases and organ rejection and in treating diseases
XX PT due to excess immune reaction
XX PS Example 2; Page 62; 71pp; Japanese.
XX CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
XX CC from humans or mice which act as regulators and drugs for sensitivity
XX CC diseases and organ rejection and in treating diseases due to excess
XX CC immune reaction, e.g. in slowing down rejection after organ transplant,
XX CC and in treating autoimmune diseases. This sequence represents the
XX CC C-terminus of the interleukin 18 binding protein encoded by the 3' end
XX CC of the gene isolated by a 3' RACE (Rapid Amplification of cDNA Ends)
XX CC reaction.
XX SQ Sequence 47 AA;

Query Match 28.0%; Score 244; DB 21; Length 47;
Best Local Similarity 100.0%; Pred. No. 4.1e-17;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 118 FSCVLVDPEDQVGRHVYLAQLMAGLRATLPPTQEALEPSSHSPPQGG 164
DB 1 fscvlvdpeqvgrhvhvylagqlwaglratlptqlealpspspqgg 47

RESULT 13
AAW98008
ID AAW98008 standard; Peptide; 40 AA.
XX
XX AAW98008;
AC
XX
XX 21-JUN-1999 (first entry)
DT
XX
XX Human interleukin-18 binding protein N-terminal peptide.
DE
XX
XX Interleukin-18 binding protein; IL-18BP; human; autoimmune disease;
XX KM inflammation; diabetes; pancreatitis; rheumatoid arthritis;
XX KM graft rejection; sepsis; chronic hepatitis; psoriasis;
XX KM inflammatory bowel disease; multiple sclerosis;
XX KM ischemic heart disease; ischemic brain injury; therapy.
XX OS Homo sapiens.
XX
XX
XX Key
XX FH Location/Qualifiers
XX FT Peptide
XX FT 1..28
XX FT /note="signal peptide"
XX FT Protein
XX FT 29..113
```

```

FT  /note= "mature protein"
XX
XX WO9909063-A1.
XX
XX 25-FEB-1999.
XX
XX 13-AUG-1998; 98WO-IL00379.
XX
XX 22-JUL-1998; 98IL-0125463.
XX 14-AUG-1997; 97IL-0121554.
XX 27-AUG-1997; 97IL-0121639.
XX 29-SEP-1997; 97IL-0121860.
XX 06-NOV-1997; 97IL-0122134.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX DiNarello C, Kim SH, Novick D, Rubinstein M;
XX
XX WPI; 1999-180975/15.
XX
XX New interleukin-18 binding protein - useful for treating human
XX diseases, including autoimmune disease and inflammation
XX
XX Claim 1; Page 63; 100pp; English.
XX
XX This polypeptide comprises the 40 N-terminal amino acids of human
XX interleukin-18 binding protein (IL-18BP) mature polypeptide. The
XX same 40-amino acid sequence is found at the N-terminus of 4 novel
XX IL-18BP splice variants (see AAW98004-007). IL-18BP polypeptides,
XX including the splice variants, that are capable of binding IL-18
XX and/or modulating and/or blocking IL-18 activity are provided.
XX Methods for their isolation and recombinant production, DNA vectors
XX expressing them, vectors useful for their expression in humans and
XX other mammals, and antibodies against them are also provided.
XX IL-18BP polypeptides, and DNA encoding them, can be used to treat
XX conditions requiring the protein (claimed). Such conditions
XX include autoimmune diseases, type I diabetes, rheumatoid arthritis,
XX graft rejections, inflammatory bowel diseases, sepsis, multiple
XX sclerosis, ischemic heart diseases, ischemic brain injury, chronic
XX hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
XX also useful for purifying IL-18 (claimed).
XX
XX Sequence 40 AA:
SQ
XX
XX Query Match 24.0%; Score 209; DB 20; Length 40;
XX Best Local Similarity 100.0%; Pred. No. 1e-13;
XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TPVSQTTTAATASVSRSTKPCSPQPPVPAKKCCPAALEVT 40
DB 1 tpvsqtttaatasvstrskpcspqppvtpaakqcpalevt 40
XX
XX RESULT 14
XX ID AAY12716 standard; Protein: 55 AA.
XX AC AAY12716;
XX
XX 21-JUN-1999 (first entry)
XX
XX Human 5' EST secreted protein SEQ ID NO:306.
XX
XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
XX forensic; gene therapy; chromosome mapping; signal peptide;
XX upstream regulatory sequence; cytokine activity; cell proliferation;
XX differentiation; haematopoiesis regulation; tissue growth regulation;
XX reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
XX thrombolytic; anti-inflammatory; tumour inhibition.
XX
XX Homo sapiens.
XX

```

```

PN WO9906549-A2.
XX
XX 11-FEB-1999.
XX
XX 31-JUL-1998; 98WO-IB01231.
XX
XX 01-AUG-1997; 97US-0905279.
XX
XX (GEST ) GENSET.
XX
XX Duclert A, Dumas Milne Edwards J, Lacroix B;
XX
XX WPI; 1999-153779/13.
XX
XX N-PSDB; AAX51494.
XX
XX New nucleic acids encoding human secreted proteins - obtained from
XX cDNA libraries derived from testis, ovary, uterus and spleen tissue
XX
XX Claim 34; Page 404-405; 522pp; English.
XX
XX AAX51459 to AAX51691 represent 5' expressed sequence tags (ESTs) for
XX human secreted proteins, and encode the proteins given in AAY12681 to
XX AAY12913, respectively. The proteins given represent the signal peptide
XX and an N-terminal fragment of a secreted protein. The nucleic acid
XX sequences can be used for producing secreted human gene products. They
XX can also be used to develop products for diagnosis and therapy. The
XX proteins obtained may have cytokine activity, cell
XX proliferation/differentiation activity, haematopoiesis regulating
XX activity, tissue growth regulating activity, reproductive hormone
XX thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and
XX activity, tumour inhibition activity or other activities. The products
XX can be used in forensic, gene therapy and chromosome mapping procedures.
XX The sequences can also be used for obtaining corresponding promoter
XX sequences. The nucleic acids encoding the signal peptide can be used for
XX directing extracellular secretion of a polypeptide or the insertion of a
XX polypeptide into a membrane, or importing a polypeptide into a cell.
XX
XX Sequence 55 AA:
SQ
XX
XX Query Match 14.0%; Score 122; DB 20; Length 55;
XX Best Local Similarity 100.0%; Pred. No. 6.7e-05;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TPVSQTTTAATASVSRSTKPCPSQ 24
DB 31 tpvsqtttaatasvstrskpcpsq 54
XX
XX RESULT 15
XX ID AAY83960 standard; Protein: 29 AA.
XX AC AAY83960;
XX
XX 28-JUL-2000 (first entry)
XX
XX Human interleukin 18 binding protein peptide fragment #8.
XX
XX Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
XX regulator; drug; sensitivity disease; organ rejection; organ transplant;
XX autoimmune disease.
XX
XX Homo sapiens.
XX
XX Key location/Qualifiers
XX MISC-difference 13..15
XX MISC-difference 17..18
XX MISC-difference 17..18
XX /note= "unknown amino acid"
XX /note= "unknown amino acid"
XX
XX WO200012555-A1.
XX

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XX 09-MAR-2000.
 PD 18-NOV-1998; 98WO-JP05186.
 XX
 PF 01-SEP-1998; 98JP-0247588.
 XX 18-NOV-1998; 98JP-0327914.
 PR
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Toriigo K, Taniai M, Kurimoto M;
 XX
 DR WPI: 2000-237850/20.
 XX
 PT Interleukin 18-binding protein with activity of regulating
 PT physiological actions of Interleukin 18, useful as regulator and drug
 PT for sensitivity diseases and organ rejection and in treating diseases
 PT due to excess immune reaction -
 XX
 PS Claim 2; Page 49; 71pp; Japanese.
 XX
 CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,
 CC and in treating autoimmune diseases. This sequence represents a peptide
 CC fragment of the human interleukin 12 receptor protein.
 XX
 SQ Sequence 29 AA;

Query Match 13.1%; Score 114; DB 21; Length 29;
 Best Local Similarity 82.8%; Pred. No. 0.00019;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 103 ALVLEQLTPALHSTNFCVLVDEPOVVOR 131
 ||||||||| | |||||||||
 Db 1 alvleqtpalhxvxfxvldpeqvqr 29

Search completed: August 19, 2002, 22:52:56
 Job time: 3842 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 19, 2002, 22:16:04 ; Search time 24.68 Seconds
(without alignments)
162.309 Million cell updates/sec

Title: US-09-786-130-1

Perfect score: 870

Sequence: 1 TPVSGTTTAAATASVRSKDP.....TLPTQEAALPSSHSPPQGG 164

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
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6: /cgn2_6/ptodata/2/1aa/backfillsl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	12.2	134	1	US-08-307-499-24
2	106	12.2	134	4	US-09-299-268-24
3	96.5	11.1	579	4	US-09-173-151A-2
4	96.5	11.1	686	4	US-09-173-151A-4
5	82.5	9.5	1241	4	US-09-040-774-2
6	79	9.1	674	3	US-08-893-852A-1
7	78	9.0	216	2	US-08-715-204-7
8	78	9.0	216	2	US-09-162-597-7
9	75	8.6	1481	2	US-08-616-844-40
10	75	8.6	1481	2	US-08-599-654-40
11	75	8.6	1481	3	US-08-944-423A-40
12	75	8.6	1481	3	US-08-944-423A-40
13	75	8.6	1481	3	US-08-944-423A-40
14	73	8.4	189	4	US-09-041-886-19
15	73	8.4	189	4	US-09-199-637A-95
16	72	8.3	280	4	US-09-247-155-178
17	71.5	8.2	1651	4	US-09-540-245A-18
18	69.5	8.0	499	4	US-09-049-672A-1
19	69	7.9	410	1	US-08-091-519-13
20	69	7.9	410	1	US-08-442-043A-13
21	69	7.9	410	5	US-09-173-151A-27
22	69	7.9	410	5	US-09-173-151A-27
23	69	7.9	410	5	US-09-173-151A-27
24	68.5	7.9	486	1	US-09-413-814-48
25	68.5	7.9	1172	1	US-07-672-483-2
26	68	7.8	372	1	US-08-313-288B-19
27	68	7.8	372	1	US-08-202-056-5
					US-08-076-093A-6

28	68	7.8	372	1	US-08-701-265-6	Sequence 6, Appli
29	68	7.8	372	2	US-08-284-586-6	Sequence 6, Appli
30	68	7.8	372	2	US-08-805-478-6	Sequence 6, Appli
31	68	7.8	372	2	US-08-802-627A-6	Sequence 6, Appli
32	68	7.8	372	2	US-08-801-238-6	Sequence 6, Appli
33	68	7.8	372	2	US-08-801-228-6	Sequence 6, Appli
34	68	7.8	372	3	US-09-104-296-6	Sequence 6, Appli
35	68	7.8	372	3	US-08-982-493-8	Sequence 8, Appli
36	68	7.8	4302	3	US-08-658-136-5	Sequence 5, Appli
37	68	7.8	4303	2	US-08-460-751-2	Sequence 2, Appli
38	67	7.7	340	4	US-09-360-779-2	Sequence 2, Appli
39	67	7.7	374	3	US-08-982-493-6	Sequence 6, Appli
40	67	7.7	623	1	US-08-653-740-7	Sequence 7, Appli
41	67	7.7	623	2	US-09-073-594-7	Sequence 7, Appli
42	67	7.7	623	3	US-09-275-925-7	Sequence 7, Appli
43	67	7.7	1257	2	US-08-750-152A-2	Sequence 2, Appli
44	67	7.7	1449	3	US-08-840-062-6	Sequence 6, Appli
45	66.5	7.6	171	4	US-09-173-151A-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-08-307-499-24
Sequence 24, Application US/08307499
Patent No. 5651972
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ. ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
TOPOLOGY: linear

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer.
APPLICANT: Zweiger, Gary B.
TITLE OF INVENTION: A NOVEL TUMOR PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,597
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/715,204
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0126 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 470373
US-09-162-597-7

Query Match 9.0%; Score 78; DB 3; Length 216;
Best Local Similarity 26.8%; Pred. No. 0.9;
Matches 26; Conservative 16; Mismatches 37; Indels 18; Gaps 4;

QY 54 LSCVACSRPNEFSILYLWLGSGFIEHLPGRLWEGSTRERGSGTQQLCKALVLEQLTPAL 113
DB .7 INFALAFAPYFTVYKISGINET-----SIIWICATA-SCGYLLTOLAKLITATFPAL 60

QY 114 HSTNFCVLVDE-----QVQRHVYLAQLMAG 141
DB 61 DSEGSFIV---PEFLKSSADIIDVIGLHILMTNPLAG 94

RESULT 9
US-08-616-844-40
Sequence 40, Application US/08616844
Patent No. 5849578
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,844
FILING DATE: 15-MAR-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-616-844-40

Query Match 8.6%; Score 75; DB 2; Length 1481;
Best Local Similarity 23.8%; Pred. No. 27;
Matches 57; Conservative 18; Mismatches 78; Indels 86; Gaps 10;

QY 2 PVSOTT-TAATVASYRSTKDCPCSPVPVPAKOCPALEV----- 39
DB 820 PVSITTSAPLSVSQTTLQSSSTPVLPRARETPVTSFOTSTVTSPTMTLHSSQTADLK 879

QY 40 --TWPEYEVPLNGTSLSCVACSRPNEFSILYLWLGSGFIEHLPGRLWEGSTRERGSGT 97
DB 880 SOSTPHQEKVITEKSPSLVS---LPTSETKAVTTNSP---LPPSLTESSTEQTLDPATS 932

QY 98 TQCLK-----ALVLE-----QLTPALHSTNFCV-----LYDEQVY-- 129
DB 933 TNLQMSPTFTTTLTKSQPLMTPTGLTSLSTASLVTGPPIAVQTAGKQLSTHPELIVPQ 992

QY 130 -----ORHVLQGLMAGL-----RATLPPTQALPSSHS-----SPQ 161
DB 993 ISTEGISTERNVIYDATTGLIPITSVPTSAREMTTKLGVTATVAPSNLSLGTSPPQ 1051

RESULT 10
US-08-599-654-40
Sequence 40, Application US/08599654
Patent No. 5882925
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,654
FILING DATE: 09-FEB-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-599-654-40

Query Match 8.6%; Score 75; DB 2; Length 1481;
Best Local Similarity 23.8%; Pred. No. 27;
Matches 57; Conservative 18; Mismatches 78; Indels 86; Gaps 10;

QY 2 PVSQTT-TAATASVSTKPCSPQPPVPAKOCPALEY----- 39
DB 820 PVSLLTSTAPLSVSQTLTPQSSSTPVLPRARETPTVSFQSTMTSFMTHLSQTDADK 879
QY 40 --TWPEVEVPLNGTSLSCVACSRPNFSILWLGNSFIEHLPRLMGSTRRGSG 97
DB 880 SOSTPHQEKVITRESKPSLVS---LPTESTKAVTTNSP---LPPLSTESSTEQTLPAITS 932
QY 98 TOLCK-----ALVLE-----QLTPALHSTNFCV-----LVDPQOV-- 129
DB 933 TNLQMSPTFTTTLIKTSQPLMTTPGTLSTASLVTPGPIAVQTAGKQLSLTHPELVPO 992
QY 130 -----QRHVYLAQLMAGL-----RATLPTQOALPSSH-----SPQ 161
DB 993 ISTEGLISTERNRVIVDATGTGLPLTSVPTSAREKMTKLGVTAEYSPASRSLSGTSPSQ 1051

RESULT 11
US-08-944-868A-40
Sequence 40, Application US/08944868A
Patent No. 6018025
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
NUMBER OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,868A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,654
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-944-868A-40

Query Match 8.6%; Score 75; DB 3; Length 1481;
Best Local Similarity 23.8%; Pred. No. 27;
Matches 57; Conservative 18; Mismatches 78; Indels 86; Gaps 10;

QY 2 PVSQTT-TAATASVSTKPCSPQPPVPAKOCPALEY----- 39
DB 820 PVSLLTSTAPLSVSQTLTPQSSSTPVLPRARETPTVSFQSTMTSFMTHLSQTDADK 879
QY 40 --TWPEVEVPLNGTSLSCVACSRPNFSILWLGNSFIEHLPRLMGSTRRGSG 97
DB 880 SOSTPHQEKVITRESKPSLVS---LPTESTKAVTTNSP---LPPLSTESSTEQTLPAITS 932
QY 98 TOLCK-----ALVLE-----QLTPALHSTNFCV-----LVDPQOV-- 129
DB 933 TNLQMSPTFTTTLIKTSQPLMTTPGTLSTASLVTPGPIAVQTAGKQLSLTHPELVPO 992
QY 130 -----QRHVYLAQLMAGL-----RATLPTQOALPSSH-----SPQ 161
DB 993 ISTEGLISTERNRVIVDATGTGLPLTSVPTSAREKMTKLGVTAEYSPASRSLSGTSPSQ 1051

RESULT 12
US-08-944-423A-40
Sequence 40, Application US/08944423A
Patent No. 6020463
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
NUMBER OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS 95

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,423A
FILING DATE: 06-OCT-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: JUN-07-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-944-423A-40

Query Match 8.6%; Score 75; DB 3; Length 1481;
Best Local Similarity 23.8%; Pred. No. 27;
Matches 57; Conservative 18; Mismatches 78; Indels 86; Gaps 10;

QY 2 PVSQTT-TAATASVSTKDCPCSPQPVFPAAKOCPALEV----- 39
DB 820 PVLITTSAPLSVSQTLTQSSSTPLPRARETPVTSFQTSMTSMTHLSSQGTADLK 879
QY 40 --TWPEVEVPLNGTSLSCVACSRFPNFSILYWLNGSFTEHLPGRLMEGSTRERGSTG 97
DB 880 SQSTPHQEKVITESKSPSLVS--LPTESTKAVTTNSP--LPSSLTESSTEQTLPATIS 932
QY 98 TOLCK-----ALYLE-----QLTPALHSTNFCV-----LYDEQVY-- 129
DB 933 TNLQMSPTTTTLTKTSQPLMTTPTGLSTSLASLVGPIAVOTTAGKQLSLTHPELIVPQ 992
QY 130 -----QRHVLAQLMAGL-----RATLPTQEOALPSSH-----SPQ 161
DB 993 ISTEGGISTERNRVIYDATGTGLPLTISVPTSAKEMTKLGVTAEYSPASHSLGTSPPQ 1051

RESULT 13
US-08-944-496-40
Sequence 40, Application US/08944496
Patent No. 6124433
GENERAL INFORMATION:
APPLICANT: PALB, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,496
FILING DATE: 06-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-944-496-40

Query Match 8.6%; Score 75; DB 3; Length 1481;
Best Local Similarity 23.8%; Pred. No. 27;
Matches 57; Conservative 18; Mismatches 78; Indels 86; Gaps 10;

QY 2 PVSQTT-TAATASVSTKDCPCSPQPVFPAAKOCPALEV----- 39
DB 820 PVLITTSAPLSVSQTLTQSSSTPLPRARETPVTSFQTSMTSMTHLSSQGTADLK 879
QY 40 --TWPEVEVPLNGTSLSCVACSRFPNFSILYWLNGSFTEHLPGRLMEGSTRERGSTG 97
DB 880 SQSTPHQEKVITESKSPSLVS--LPTESTKAVTTNSP--LPSSLTESSTEQTLPATIS 932
QY 98 TOLCK-----ALYLE-----QLTPALHSTNFCV-----LYDEQVY-- 129
DB 933 TNLQMSPTTTTLTKTSQPLMTTPTGLSTSLASLVGPIAVOTTAGKQLSLTHPELIVPQ 992
QY 130 -----QRHVLAQLMAGL-----RATLPTQEOALPSSH-----SPQ 161
DB 993 ISTEGGISTERNRVIYDATGTGLPLTISVPTSAKEMTKLGVTAEYSPASHSLGTSPPQ 1051

RESULT 14
US-09-041-886-19
Sequence 19, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
TITLE OF INVENTION: Rabizadeh, Sharrow
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO. 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-041-886-19

Query Match 8.5%; Score 74; DB 4; Length 1312;
Best Local Similarity 26.7%; Pred. No. 30;
Matches 47; Conservative 20; Mismatches 75; Indels 34; Gaps 9;

QY 2 PVSQTTAATAASVSTKDP-C-PSQPPVPAKQCPALEVTWPEVPLNGTILSLCVACS 60
DB 570 PNSTLPPRAATPTPPSPRPSRPSHPAHGSPAPVSTMPK-RMSSEGPSPRMKAQR 628
QY 61 REPNSILYWGNGS-----FIEHLPGRLMEGST--SRERGSTGQLCKALVLEQLTP 111
DB 629 HPRNRHV--AGRGSISSGLEFVSHNPPS--EAAIPVAKTSPSGTWSVYSGVPRLSP 684
QY 112 ALHSTFSCVLDPEQVVRHV-----VLAQLMAGLRATLPQOALPSSHSP 160
DB 685 KTHR-----PRSPRQNSIGNTPSGPVLASPQAGT---IPTAVAMPTPAASP 728

RESULT 15
US-09-199-637A-95
; Sequence 95, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-95

Query Match 8.4%; Score 73; DB 4; Length 189;
Best Local Similarity 23.4%; Pred. No. 2.6;
Matches 44; Conservative 20; Mismatches 64; Indels 60; Gaps 10;

QY 1 TPVSQTTAATAASVSTKDPSPVPAKQCPALEVTWPEVPLNGTILSLCVACS 60

DB 24 SPASATTAASA-----PASTACSPALRLAA-----SATPALAFSCS 63
QY 61 REPNSILYWGNGS-----FIEHLPGRLMEGST--SRERGSTGQLCKALVLEQLTP 104
DB 64 SW-NFQTSMAIRGSMNATRIPTHLPSHGVLSDDIAVARSSPTNRQSKSMDGNLGCAS 122
QY 105 -----VLEQLTPALH-----STNFSCVLDPEQVVRHVYLAQLMAG--LRATLPPTQ 150
DB 123 SSPGCVLPFTASISAHSAALKSKSNF--FTSPRSIEYR-----WTADVFPPLLAFTK 173
QY 151 EALPSSHS 158
DB 174 IEISSSS 181

Search completed: August 19, 2002, 22:53:42
Job time: 2258 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 22:46:54 ; Search time 43.03 Seconds
(without alignments)
366.225 Million cell updates/sec

Title: US-09-786-130-1

Perfect score: 870
Sequence: 1 TPVSQTTTAAATASVRSWKDP.....TLPPQTQALPSSHSPPQGG 164

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	205	23.6	235	2 T30656	hypothetical prote
2	164	18.9	133	2 T30655	hypothetical prote
3	104.5	12.0	120	2 T30769	hypothetical prote
4	94.5	10.9	126	2 E36837	D5L protein - vari
5	93.5	10.7	126	2 T28442	hypothetical prote
6	92.5	10.6	138	2 F72150	B6L protein - vari
7	92.5	10.3	138	2 C49276	16k protein - Ectr
8	89.5	9.7	286	2 C85061	Ig heavy chain pre
9	84.5	9.5	370	2 S64067	probable phosphati
10	83	9.5	1241	2 T37190	tRNA-pseudouridine
11	82.5	9.5	1241	2 T37190	nephritin - human
12	82.5	9.5	2043	2 T18524	scavenger receptor
13	81	9.3	627	2 T27123	hypothetical prote
14	81	9.3	1420	2 T17158	CL2AB protein - ra
15	81	9.3	1435	2 T46611	CL2BB protein - ra
16	81	9.3	1452	2 T17157	CL2BA protein - ra
17	81	9.3	1463	2 T17159	CL2AC protein - ra
18	81	9.3	1467	2 T17160	CL2BC protein - ra
19	81	9.3	1478	2 T17185	CL2CA protein - ra
20	81	9.3	1487	2 T14324	alpha-latrotoxin r
21	80	9.2	359	2 S43787	serine/threonine-r
22	79.5	9.1	578	2 AC0179	probable exported
23	79	9.1	628	2 D86466	kinase-related pro
24	78.5	9.0	2594	2 A35774	hypothetical prote
25	78	9.0	216	2 T27851	hypothetical prote
26	78	9.0	1851	2 T19964	tetratricopeptide
27	77.5	8.9	596	2 G75457	transcription fact
28	77.5	8.9	754	2 S37403	tenascin Y precurs
29	77.5	8.9	1914	2 T42635	

30	77	8.9	120	2 T30653	hypothetical prote
31	76.5	8.8	578	2 AG0119	probable OmpA-fam1
32	76.5	8.8	1651	2 T14160	transmembrane rece
33	76	8.7	374	2 S32785	G protein-coupled
34	75.5	8.7	535	2 C83395	probable acyl-CoA
35	75.5	8.7	1318	2 T05745	hypothetical prote
36	75	8.6	504	2 JQ2151	matling-type locus
37	74.5	8.6	416	2 S33473	interleukin-1 rece
38	74.5	8.6	430	2 F96686	unknown protein F1
39	74.5	8.6	660	2 JMW067	chitinase (EC 3.2.
40	74.5	8.6	819	2 T05744	hypothetical prote
41	74.5	8.6	1612	2 T30805	dufil protein - mo
42	74.5	8.6	3511	2 A59295	unconventional myo
43	74	8.5	547	2 G75364	DNA mismatch repair
44	73.5	8.4	353	1 A1HU	Ig alpha-1 chain C
45	73.5	8.4	354	2 AF1051	conserved hypothet

ALIGNMENTS

Query Match	Score	DB 2	Length	235
Best local Similarity	38.1%	Pred. No. 1.3e-11		
Matches	51	Conservative	22	Mismatches 49; Indels 12; Gaps 5
QY	27	VFPAAKQCPALVETWPEVEYPLNGTSLSCVACSRFPNFSILYWGSGFIEHLPGLME	86	
DB	29	LFLYSRAC-ELEIS--TQVGNGTTLTCTGCTNHTHVSILYIVNESPEDQDSSLSL	84	
QY	87	GSTRER--GSTGTOLCKALVLEQITPALSHTNFCVLPDEQVQRRHVLAQLMAGLRA	144	
DB	85	GRHKHKRFPNQSLEISTNLTGCP-DVATHSTNFCVLPDEQVQRRHVLAQLMAGLRA	144	
QY	145	TLPPQTQALPSSHS 158		
DB	139	TLPPQTATRPPENA 152		
RESULT	2			
T30655				
hypothetical protein 53L - Molluscum contagiosum virus 1				
N:Alternate names: MC053L				
C:Species: Molluscum contagiosum virus 1				
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000				
R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.				
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific				
A:Reference number: Z20876; MUID:96325459				
A:Accession: T30655				
A>Status: preliminary; translated from GB/EMBL/DBJ				
A:Molecule type: DNA				
A:Residues: 1-133 <SEN>				


```
QY 106 LEQLTPA-----LHSTNSCVLVDPQVVRHVLQAQLMAGIRATLPP 148
      : | : | : | : | : | : | : | : | : | : | : | : |
Db 239 VSQASPGWICVRHGSFML-----HQIRRMVALAVLAA--RCQLPP 278
```

RESULT	11
T37190	

nephrin - human
C:Species: Homo sapiens (man)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T37190
R:Kestila, M.; Lehtkeri, U.; Mannikko, M.; Lamedin, J.; McCreedy, P.; Putaala, H.; Ruoto-
nen, K. J. *Proc Natl Acad Sci USA* 96:1002-1006 (1999)

A:Title: Positionally cloned gene for a novel glomerular protein - nephrin - is mutated
 A:Reference number: 221629; MUID:98325371
 A:Accession: T37190
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1241 <KES>
 A:Cross-references: EMBL:AF035635; NID:g3025698; PIDN:AAC39667.1; PID:g3025699
 C:Genetics:
 A:Map position: 19
 A:Note: mutated in congenital nephrotic syndrome of the Finnish type (NPHS1); located in

Query Match	9.5%	Score	82.5	DB	2	Length	1241
Best Local Similarity	21.2%	Pred. No.	18				
Matches	38	Conservative	16	Mismatches	58	Indels	67
						Gaps	7

QY 22 PSQPEVPAKQCPALEVMP---EVEEPLNGTSLSCVACSNFPNFSILYWLGNCSFIE 78
 | ||| | : || ||| | : || |||
 330 HPGQVY-----YKPDGKPDWVGGGQV-----

0Y 79 HLPRIWEGSTREKSTGTQ-LCKALVLEQLPALHSTNESC----- 12

204	-----FVSIAMGIEHTIQAIVAKSVLVMIVKRPEDHGAQJLSCFAHNSVBAQIQEHGITLE	33
205	-----	
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348	-----	</

Db 335 QVTFPPSAIIILGASQTEKNKVTLSGVSKSSRPVLLRWLGLWRQLPMEETVMDGLH 393

RESULT	12
118524	

C;Species:	Geodia cydonium	protein	homolog	blotting	geodia cydonium
C;Date:	15-Oct-1999	#sequence	15-Oct-1999	#text	chance 11-May-2000

R.; Blumberg, B.; Pancer, Z.; Diehl-Seifert, B.; Steffen, R.; Muenkner, J.; J. Cell Sci. 111, 2635-2644, 1998

A;Reference number: Z18947; MUID:98369060
A;Accession: T18524

A;Molecule type: mRNA
A;Residues: 1-2043 <BLU>

C;Genetics:
A;Gene: SRCRM2

Query Match	9.58;	Score 82.5;	DB 2;	Length 2043;.
-------------	-------	-------------	-------	---------------

Matches	36;	Conservative	22;	Mismatches	65;	Indels	33;	Gaps	
---------	-----	--------------	-----	------------	-----	--------	-----	------	--

Db 1765 CSREPT-----KCPFLISDHTVASSSETTINIVSFTC-----DNGYFLKGDKI 1811

```
09 // IEHLPGRLWGSTSRERESTGTOLCALVL-EQUTPALHSINFSCVLA---DPEOVQR 131
```

Db 1811 LECSTGWMNSTAPT---CSLPSCSCLKSDHVTAASSDITDINAMVITFCDDRTYLING 1867

Qy 132 HVLA-----QLMAGLRAT---LPPTQALPSSHSPP 160
:::| :| | | :| | | | |

Db 1868 NKIIACSTGWMNSTAPTCKEIPTCCELPSSVAP 1903

RESULT 13

hypothetical protein Y53C10A.10 - *Caenorhabditis elegans*
 T27123
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T27123
 R:White, S.
 submitted to the EMBL Data Library, November 1998

A:Accession: T27123
A:Status: preliminary; translated from GB/EMBL/DBJ

A/Residues: 1-627 <WIL>
A/Cross-references: EMBL:AL033536. PIDN:CAA22144.1: CESP:Y53C10A.10

C;Genetics:
A;Gene: CESP:Y53C10A.10

A1Gene: CESP.Y53C10A.10
A1Introns: 12/1; 82/1; 102/1; 131/1; 181/1; 212/1; 236/3; 308/3; 351/3; 382/3; 426/1

Query Match	9.3%	Score 81	DB 2	Length 627
Best Local Similarity	24.5%	Pred. No. 11		
Matches 39	Conservative 20	Mismatches 40	Indels 60	Gaps 8

[illegible]

07 76 --FIEHLPGR---LMEGSTRERGSTGTOLCKALVLEQITPAHSTNESCVLVDPQOVQ 130

404	VALLEYFPGGVYKNGIDBADE-SSGSSLSNS	-----	1PSP LSPIDS-----	443
DU				
0V	131 RHVVI AOTWAGT BATT.DP-----	-----	TOFAT PSCUSSD 160	

```

Db      446 -----LTATTPPGSTQAASTTESAMASSIESP 473

```

RESULT 14
T17158

C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 18-Feb-2000

R; Sugita, S.; Ichtchenko, K.; Khvotchev, M.; Sudhof, T.C. submitted to the EMBL Data Library, July 1998

A;Reference number: 218712
A;Accession: T17158

A:Molecule type: mRNA
A:Residues: 1-1420 <SUG>

C; Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match	9.38;	Score 81;	DB 2;	Length 1420;
Best Local Similarity	23.88;	Pred. No. 29;		

2 PYSQTTTATASVSTKDP-----CPSQPVEFPAKQ-CPALE---VTWPE-----V 44

Dd 433 PVSSTVAGPQESRGTKRPDAVSTTKIPVTNIEPLPERCEALEMKGIKMPQTRGMNV 4922

Db 493 ERPEPKGTRGASVLCMASTGTWNPGRPDLSNCTSHWVNLQAQKIRSGENAAASLANELAK 552

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 19, 2002, 22:52:59 ; Search time 23.86 Seconds

(without alignments)
266.136 Million cell updates/sec

Title: US-09-786-130-1
Perfect score: 870
Sequence: 1 TPVSGTTTAAATASVRSKDP.....TLRPTQALPSSHSPPQOG 164

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt-40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74.2	85.3	197	118B_HUMAN	O95998 homo sapien
2	106	12.2	134	1VC09_SPKA	P32223 swinepox vi
3	83	9.5	370	PUS2_YEAST	P53167 saccharomyc
4	81	9.3	823	DMSA_RHOCA	052675 rhodobacter
5	78.5	9.0	2594	7LRS_DROVI	P20806 drosophila
6	77.5	8.9	754	MBPL_KIOLA	P39679 Kluveromyc
7	76.5	8.8	1914	1KMUS_HUMAN	Q15746 homo sapien
8	76	8.7	374	CCR5_RAT	P34997 rattus norv
9	75.5	8.7	505	1CXAA_MOUSE	O92794 rattus norv
10	75.5	8.7	2004	MOZ_HUMAN	P43303 rattus norv
11	74.5	8.6	416	1ILIS_RAT	O94224 mus musculu
12	74.5	8.6	3511	MY15_MOUSE	P01876 homo sapien
13	73.5	8.4	353	1ALCI_HUMAN	P03350 mus musculu
14	73.5	8.4	1172	1TSP2_MOUSE	P30015 escherichia
15	73	8.4	1538	1LHR_ECOLI	004538 t genome po
16	73	8.4	3415	1POLG_POWVL	P26414 microspor
17	72.5	8.3	456	1GUNA_MICBI	P76594 escherichia
18	72	8.3	886	1YFIO_ECOLI	O94664 mus musculu
19	71.5	8.2	423	1GATM_MOUSE	Q04317 caenorhabd
20	71.5	8.2	780	1NH48_CAEEL	003172 mus musculu
21	71.5	8.2	2688	1ZEPI_MOUSE	P20758 gorilla gor
22	70.5	8.1	353	1ALCI_GORGO	O94638 t genome po
23	70.5	8.1	633	1CNEI_HUMAN	P26414 microspor
24	70	8.0	2090	1HRC1_MESAU	P76594 escherichia
25	69.5	8.0	583	1HEMO_BRARE	O94664 mus musculu
26	69.5	8.0	4590	1FATR_HUMAN	Q04317 caenorhabd
27	69	7.9	410	1ILIS_MOUSE	003172 mus musculu
28	68.5	7.9	423	1GATM_MOUSE	P20758 gorilla gor
29	68.5	7.9	486	1ENV_HTLV2	O94638 t genome po
30	68.5	7.9	1172	1TSP2_MOUSE	P26414 microspor
31	68	7.8	372	1CCR5_HUMAN	P76594 escherichia
32	68	7.8	626	1MAG_HUMAN	O94664 mus musculu
33	68	7.8	1257	1KPBA_CAEEL	Q04317 caenorhabd

34	68	7.8	4303	1PKD1_HUMAN	P98161 homo sapien
35	67.5	7.8	354	1YJFR_ECOLI	P39300 escherichia
36	67.5	7.8	488	1ENV_HTLIF	003817 human t-cel
37	67.5	7.8	488	1ENV_HTLIM	P23064 human t-cel
38	67.5	7.8	488	1ENV_HTLIN	003816 human t-cel
39	67.5	7.8	976	1KEMS_MOUSE	P09561 mus musculu
40	67.5	7.8	978	1KEMS_RAT	000495 rattus norv
41	67.5	7.8	1025	1HIRA_FUGRU	042611 fugu rubrip
42	67.5	7.8	1522	1BA13_HUMAN	O60242 homo sapien
43	67	7.7	374	1CCR5_MOUSE	O04683 mus musculu
44	67	7.7	564	1PKNA_ANASP	P54734 anabena sp
45	67	7.7	690	1TOP1_BACHD	O9ka23 bacillus ha

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	197 AA.
ID	118B_HUMAN			
AC	O95998: O96027: O95993:			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-18 binding protein precursor (IL-18BP).			
GN	IL18BP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99146382; PubMed=10023777;			
RA	Novick D., Kim S.-H., Fantuzzi G., Reznikov L.L., Dinarello C.A.,			
RT	Rubinstein M.;			
RT	"Interleukin-18 binding protein: a novel modulator of the Th1 cytokine			
RL	response.";			
RL	Immunity 10:127-136(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99192308; PubMed=10094485;			
RA	Alizawa Y., Akita K., Tanai M., Torioge K., Mori T., Nishida Y.,			
RT	Ushio S., Nukada Y., Tanimoto T., Ikegami H., Ikeda M., Kurimoto M.;			
RT	"Cloning and expression of interleukin-18 binding protein.";			
RL	FEBS Lett. 445:338-342(1999).			
CC	-1- FUNCTION: FUNCTIONS AS AN INHIBITOR OF THE EARLY TH1 CYTOKINE			
CC	RESPONSE.			
CC	-1- SUBUNIT: BINDS TO IL-18.			
CC	-1- SUBCELLULAR LOCATION: Secreted (Potential).			
CC	-1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A/IL-18BP, B/IL-18BP AND C/IL-			
CC	18BP (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; AF110798; AAD17187.1; -			
DR	EMBL; AF110798; AAD17188.1; -			
DR	EMBL; AF110798; AAD17189.1; -			
DR	EMBL; AF110799; AAD17190.1; -			
DR	EMBL; AF110800; AAD17191.1; -			
DR	EMBL; AF110801; AAD17192.1; -			
DR	MM; 604113; -			
DR	InterPro: IPR003006; Ig_MHC.			
DR	Pfam: PF00047; 19; 1.			
KT	Immunoglobulin domain; Glycoprotein; Signal; Alternative splicing.			
FT	SIGNAL 1 28 POTENTIAL.			

FT CHAIN 29 197 INTERLEUKIN-18 BINDING PROTEIN.
 FT DOMAIN 77 155 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 84 148 BY SIMILARITY.
 FT CARBOHYD 77 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 168 197 VRSPPRGQEDPELCFHWGKGLQSSSL -> AGLRATL
 FT VARSPLIC 77 113 PPTQALPSSSHSSPOQOG (IN ISOFORM A).
 FT VARSPLIC 77 113 NGTLTSLSCVACSRFPNFSILYWLNGSFIEHLPGRLW ->
 FT VARSPLIC 77 113 SWAEGNLAHPHRSPPALQPOQSTAAGLRLSTGPAAQ (IN
 FT VARSPLIC 114 197 ISOFORM B).
 FT VARSPLIC 197 AA: 21698 MW: FLD626AB2B285E1 CRC64:
 SO SEQUENCE

Query Match 85.3%; Score 742; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. No. 1.8e-66;
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPVSTTTAATASVSTKDPSPPPVPAKOCALVETPEVEVPLNGTSLSCVACS 60
 DB 29 TPVSTTTAATASVSTKDPSPPPVPAKOCALVETPEVEVPLNGTSLSCVACS 88
 QY 61 RFPNFSILYWLNGSFIEHLPGRLWEGSTSRGSGTGLCALVLEQLPALHSTNESC 120
 DB 89 RFPNFSILYWLNGSFIEHLPGRLWEGSTSRGSGTGLCALVLEQLPALHSTNESC 148
 QY 121 VLVDPEQVQVRHVVLAQLM 139
 DB 149 VLVDPEQVQVRHVVLAQLM 167

RESULT 2
 VC09_SPVKA STANDARD; PRT: 134 AA.
 ID VC09_SPVKA
 AC P32223;
 DT 01-OCT-1993 (Rel. 27, Created)
 DR 01-OCT-1993 (Rel. 27, Last sequence update)
 DE 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Hypothetical protein C9.
 GN C9L.
 OS Swinepox virus (strain Kasza) (SPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Suipoxvirus.
 OX NCBI_TaxId=10277;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9406924; PubMed=8249275;
 RA Messing R.F., Jayarama V., Moyer R.W.;
 RT "DNA sequence analysis of conserved and unique regions of swinepox
 RT virus: identification of genetic elements supporting phenotypic
 RT observations including a novel G protein-coupled receptor
 RT homologue.";
 RL Virology 197:511-528(1993).
 CC -----
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 CC
 CC EMBL: L22013; AAC37862.1; -;
 DR Hypothetical protein.
 KW
 SO SEQUENCE 134 AA: 15811 MW: F3528BB783ED1DC4 CRC64:

Query Match 12.2%; Score 106; DB 1; Length 134;
 Best Local Similarity 28.4%; Pred. No. 0.001;
 Matches 27; Conservative 20; Mismatches 42; Indels 6; Gaps 3;

QY 57 VACSRFPN--FSLIWL--GNGSFIEHLPGRLWEGS--TSRERGSGTGLCALV
 DB 38 VACNGYNTSTYSILYWMVGNNTFEQLMSDHYKKEKYNSTERNHEMYRLTDLII
 QY 111 PALHSTNFSVCVLDPEQVQVRHVVLAQLMAGLRAT 145
 DB 98 SEEMTKLTCTVLSLDIYTPIKASITILNLMSCLTPT 132

RESULT 3
 PUS2_YEAST STANDARD; PRT: 370 AA.
 ID PUS2_YEAST
 AC P53167; Q06713;
 DT 01-OCT-1996 (Rel. 34, Created)
 DR 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Pseudouridylate synthase 2 (EC 4.2.1.70) (Pseudouridine synthase 2).
 GN PUS2 OR YG1063W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxId=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96208513; PubMed=8641292;
 RA Simos G., Tekotte H., Grosjean H., Segref A., Sharma K., Tollervey D.,
 RA Hurt E.C.;
 RT "Nuclear pore proteins are involved in the biogenesis of functional
 RT tRNA.";
 RL EMBO J. 15:2270-2284(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=97377993; PubMed=9234674;
 RA Feuerann M., de Montigny J., Potier S., Souciet J.-L.;
 RT "The characterization of two new clusters of duplicated genes
 RT suggests a 'leugo' organization of the yeast Saccharomyces cerevisiae
 RT chromosomes.";
 RL Yeast 13:861-869(1997).
 CC -1- FUNCTION: FORMATION OF PSEUDOURIDINE IN THE ANTICODON STEM AND
 CC LOOP OF TRANSFER RNAs.
 CC -1- CATALYTIC ACTIVITY: Uridyl + D-ribose 5-phosphate -> pseudouridine
 CC 5'-phosphate + H(2O).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE TRNA FAMILY OF PSEUDOURIDINE SYNTHASES.
 CC
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 CC
 CC EMBL: X80674; CAA56699.1; -;
 DR EMBL: Z72585; CAA96766.1; -;
 DR SGD: S0003031; PUS2.
 DR InterPro: IPR001406; Pseudou_synth_1.
 DR Pfam: PF01416; Pseudou_synth_1; 1.
 KW Lysase; tRNA processing; Nuclear protein.
 FT CONFLICT 136 136 C -> S (IN REF. 2).
 SO SEQUENCE 370 AA: 41891 MW: 776D3A5DB8C35BC3 CRC64:

Query Match 9.5%; Score 83; DB 1; Length 370;
 Best Local Similarity 29.6%; Pred. No. 0.68;
 Matches 32; Conservative 18; Mismatches 36; Indels 22; Gaps 6;

QY 48 LNSTLSLSCVACSRFPN--SILYWLNGSFIEHLPGRLWEGSTSRGSGTGLCALV 105
 DB 186 LSGTISGVCCLPSKDAEAMQEVGTHNFHTTGLW-GDSQAQNH-----IKNVV 238
 QY 106 LEQLTPA-----LHSTNFSVCVLDPEQVQVRHVVLAQLMAGLRATLP 148

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Db      239 VSQSPGWCIVRHQSGFML-----HQIRRMVALAVLA--RCQLPP 278

RESULT 4
DMSA_RHOCA STANDARD; PRT; 823 AA.
AC 052675;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dimethyl sulfoxide reductase precursor (EC 1.8.99.-) (DMSO reductase)
DE (DMSOR).
GN DORA.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata)
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
ON NCBI_TaxID=1061;
RX 11
SEQUENCE FROM N.A., AND SEQUENCE OF 43-59.
RP STRAIN=DSM 938 / 37B4;
RC MEDLINE=97008997; PubMed=8850107;
RC MEDLINE=97008997; PubMed=8850107;
RC SHAW A.L., HANSON G.R., MCEWAN A.G.;
RT 'Cloning and sequence analysis of the dimethylsulfoxide reductase
RT structural gene from Rhodobacter capsulatus.';
RL Biochim. Biophys. Acta 1276:176-180(1996).
RN 12]
REVIEWS.
RA SHAW A.L., MCEWAN A.G.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN 13]
X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
RP STRAIN=DSM 938 / 37B4;
RC MEDLINE=97045990; PubMed=8890912;
RC SCHNEIDER F., LOEWE J., HUBER R., SCHINDLIN H., KISKER C.,
RA KRAEBELIN J.;
RT 'Crystal structure of dimethyl sulfoxide reductase from Rhodobacter
RT capsulatus at 1.88-A resolution.';
RL J. Mol. Biol. 263:53-69(1996).
RN 14]
X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RP STRAIN=H123;
RC MALPINE A.S., MCEWAN A.G., SHAW A.L., BAILEY S.;
RT 'Molybdenum active centre of DMSO reductase from Rhodobacter
RT capsulatus: crystal structure of the oxidised enzyme at 1.82-A
RT resolution and the dithionite-reduced enzyme at 2.8-A resolution.';
RL J. Biol. Inorg. Chem. 2:690-700(1997).
RN 15]
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RP STRAIN=H123;
RC MEDLINE=20296793; PubMed=10835270;
RA STEWART L.J., BAILEY S., BENNETT B., CHARNOCK J.M., GARNER C.D.,
RA MALPINE A.S.;
RT 'Dimethylsulfoxide reductase: an enzyme capable of catalyzes with
RT either molybdenum or tungsten at the active site.';
RL J. Mol. Biol. 299:593-600(2000).
RN 16]
X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RP STRAIN=H123;
RC MEDLINE=20442077; PubMed=10885771;
RA BRAY R.C., ADAMS B., SMITH A.T., BENNETT B., BAILEY S.;
RT 'Reversible dissociation of thiolate ligands from molybdenum in an
RT enzyme of the dimethyl sulfoxide reductase family.';
RL Biochemistry 38:11258-11269(2000).
RN 17]
FUNCTION: TERMINAL REDUCTASE DURING ANAEROBIC GROWTH ON
CC VARIOUS SULFOXIDE AND N-OXIDE COMPOUNDS.
CC CATALYTIC ACTIVITY: REDUCES VARIOUS N-OXIDE AND SULFOXIDE
CC COMPOUNDS INCLUDING TRIMETHYLAMINE N-OXIDE.
CC -1- COPACITOR: MOLYBDENUM (MOLYBDOPTERIN).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
CC OXIDOREDUCTASE FAMILY.

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CC or send an email to license@sdb-sdb.ch).
CC -----
CC EMBL; U49506; AAD13674.1; -.
DR PDB; 1DMR; 18-MAR-98.
DR PDB; 2DMR; 18-MAR-98.
DR PDB; 3DMR; 18-MAR-98.
DR PDB; 4DMR; 18-MAR-98.
DR PDB; 1E18; 11-JUN-00.
DR PDB; 1E5V; 25-AUG-00.
DR PDB; 1E60; 25-AUG-00.
DR PDB; 1E61; 25-AUG-00.
DR InterPro; IPR001467; Molybdopterin.
DR Pfam; PF00384; molybdopterin; 1.
DR PROSITE; PS00551; Molybdopterin_PROK_1; FALSE_NEG.
DR PROSITE; PS00490; Molybdopterin_PROK_2; 1.
DR PROSITE; PS00932; Molybdopterin_PROK_3; FALSE_NEG.
KW Oxidoreductase; Molybdenum; Periplasmic; Signal; 3D-structure.
FT SIGNAL 1 44
FT CHAIN 45 823 DIMETHYL SULFOXIDE REDUCTASE.
FT ACT_SITE 189 189
FT CONFLICT 81 81
FT CONFLICT 85 85 T -> S (IN PDB ENTRY).
FT CONFLICT 149 149 E -> A (IN PDB ENTRY).
FT CONFLICT 149 149 Q -> E (IN PDB ENTRY).
FT CONFLICT 276 278 DHV -> EHI (IN PDB ENTRY).
FT CONFLICT 322 322 M -> D (IN PDB ENTRY).
FT CONFLICT 336 337 SD -> EG (IN PDB ENTRY).
FT CONFLICT 354 354 I -> E (IN PDB ENTRY).
FT CONFLICT 416 416 I -> A (IN PDB ENTRY).
FT CONFLICT 498 498 I -> V (IN PDB ENTRY).
FT CONFLICT 568 568 K -> A (IN PDB ENTRY).
FT CONFLICT 597 597 E -> Q (IN PDB ENTRY).
SQ SEQUENCE 823 AA; 89561 MW; 0B5E901CF2D69273 CRC64;

Query Match 9.3%; Score 81; DB 1; Length 823;
Best Local Similarity 32.8%; Pred. NO. 2.8;
Matches 22; Conservative 7; Mismatches 26; Indels 12; Gaps 3;

QY 16 STKRP---CSPQPPFPAPAKOCAPALEVWPEVEVPLNLTLSLSCVACSRPFSILYWG 72
DB 424 ATKGPFWLAAAGASVTPAVRVDMLEN--PGAEDFENGTR-----SKFPVKMAWVG 474
QY 73 NGSFIEH 79
DB 475 GNPVHH 481

RESULT 5
ID 7LES_DROVI STANDARD; PRT; 2594 AA.
AC P20806;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sevenless protein (EC 2.7.1.112).
GN SEV.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriodea; Drosophilidae; Drosophila.
OX NCB1_Taxid=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319110; PubMed=2115169;
ZA Michael W.M., Bowtell D.D.L., Rudin G.M.;

```

RT "Comparison of the sevenless genes of Drosophila virilis and
 RL Drosophila melanogaster.";
 CC Proc. Natl. Acad. Sci. U.S.A. 87:5351-5353(1990).
 CC -1- FUNCTION: RECEPTOR FOR AN EXTRACELLULAR SIGNAL REQUIRED TO
 CC INSTRUCT A CELL TO DIFFERENTIATE INTO A R7 PHOTORECEPTOR. THE
 CC LIGAND FOR SEV IS THE BOSS (BRIDE OF SEVENLESS) PROTEIN.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES. SEVENLESS SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- CAUTION: UNCLEAR WHETHER THE POTENTIAL MEMBRANE SPANNING REGION
 CC NEAR THE N-TERMINUS IS PRESENT AS A TRANSMEMBRANE DOMAIN IN THE
 CC NATIVE PROTEIN OR SERVES AS A CLEAVED SIGNAL SEQUENCE.

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 DR EMBL: M34545; AAA28883.1; -;
 DR EMBL: M34544; AAA28883.1; JOINED.
 DR EMBL: M34543; AAA28883.1; JOINED.
 DR PIR: A35774; A35774.
 DR HSSP: P11362; IFGK.
 DR FLYBASE: FBgn0013140; Df1r\sev.
 DR InterPro: IPR000719; Euk_kinase.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR000033; Ldl_receptor_rep.
 DR InterPro: IPR002011; Receptor_ty_r_kin_II.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00041; fn3; 6.
 DR Pfam: PF00069; Pkinase; 1.
 DR SMART: SM00060; FN3; 5.
 DR SMART: SM00135; LY; 1.
 DR SMART: SM00219; TYKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
 KW Phosphorylation; Receptor; Vision; Repeat.
 FT DOMAIN 1 2139
 FT TRANSEM 2140 2163
 FT DOMAIN 2164 2594
 FT DOMAIN 9 26
 FT DOMAIN 356 459
 FT DOMAIN 464 555
 FT DOMAIN 835 935
 FT DOMAIN 1328 1421
 FT DOMAIN 1706 1816
 FT DOMAIN 1817 1916
 FT DOMAIN 1917 2007
 FT DOMAIN 2057 2063
 FT DOMAIN 2224 2495
 FT NP_BIND 2230 2238
 FT BINDING 2257 2257
 FT MOD_RES 2291 2391
 FT CARBOHYD 77 77
 FT CARBOHYD 401 401
 FT CARBOHYD 508 508
 FT CARBOHYD 532 532
 FT CARBOHYD 641 641
 FT CARBOHYD 667 667
 FT CARBOHYD 778 778
 FT CARBOHYD 797 797
 FT CARBOHYD 874 874
 FT CARBOHYD 980 980
 FT CARBOHYD 1257 1257
 FT CARBOHYD 1344 1344

FT CARBOHYD 1382 1382 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1577 1577 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1587 1587 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1657 1657 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1752 1752 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1776 1776 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1824 1824 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1908 1908 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1966 1966 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2088 2088 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 2594 AA; 289130 MW; 77DBA356CBAD0BBD CRC64;
 Query Match 9.0%; Score 78.5; DB 1; Length 2594;
 Best Local Similarity 23.6%; Pred. No. 20;
 Matches 30; Conservative 22; Mismatches 44; Indels 31; Gaps 5;
 OY 51 TSLSCVACSRP-----NFTLYVLGNSFTLEHPLGRLMESTSRE----- 92
 DB 2205 SSSLSDADIALPQIMNKRITLRLFLGSAF-----GEVYESQLOAEDEBAPQRYAISKSL 2259
 OY 93 -RGSTGTOLKALVLEOLTPALHSTNFSCVL-----VPEQVQRRHVYLAQLMAGLRATL 146
 DB 2260 RKGA--SEFALDLQALMSNFKHNTVYCLIGCDTDSISLIMHMEAGDLSYLRAR 2317
 OY 147 PPTQDAL 153
 DB 2318 PSSQDAL 2324
 RESULT 6
 MBP1_KLULA
 ID MBP1_KLULA STANDARD; PRT; 754 AA.
 AC P39679;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Transcription factor MBP1 (MBF subunit P120).
 GN MBP1.
 OS Kluyveromyces fragilis (Yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxId=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93383264; PubMed=8372350;
 RA Koch C., Moll T., Neuberg M., Ahorn H., Nasmyth K.;
 RT "A role for the transcription factors Mbpl and Sw14 in progression
 RT from G1 to S phase.";
 RL Science 261:1551-1557(1993).
 CC -1- FUNCTION: BINDS TO MCB ELEMENTS (MLU I CELL CYCLE BOX) FOUND IN
 CC THE PROMOTER OF MOST DNA SYNTHESIS GENES. TRANSCRIPTIONAL
 CC ACTIVATION BY MBF HAS AN IMPORTANT ROLE IN THE TRANSITION FROM G1
 CC TO S PHASE. IT MAY HAVE A DUAL ROLE IN THAT IT BEHAVES AS AN
 CC ACTIVATOR OF TRANSCRIPTION AT THE G1-S BOUNDARY AND AS A REPRESSOR
 CC DURING OTHER STAGES OF THE CELL CYCLE.
 CC -1- SUBUNIT: MBF CONTAINS SW16 AND MBP1.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.

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 DR EMBL: X74159; CA52272.1; -;
 DR PIR: S37403; S37403.
 DR HSSP: P39678; 1BM8.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR003163; Yeast_DNA_bind.

DR EMBL: AF096769; AAD51381.1; JOINED.
DR EMBL: AF096770; AAD51381.1; JOINED.
DR EMBL: X90870; CA62378.1; -.
DR HSSP: P56276; IRLK.
DR MIM: 600922; -.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR003598; I9_C2.
DR InterPro: IPR003600; I9_Like.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00047; I9; 8.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00014; FNTYPEIII.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00410; IG_Like; 1.
DR SMART: SM00408; IGC2; 8.
DR SMART: SM00220; S_Itc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
KW Alternative Initiation; Alternative splicing.
FT CHAIN 1 1914
FT MYOSIN LIGHT CHAIN KINASE, NON-MUSCLE
FT ISOZYME.
FT CHAIN 923 1914
FT MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT ISOZYME.
FT CHAIN 1761 1914
FT INIT_MET 923 923
FT INIT_MET 1761 1761
FT DOMAIN 1343 1713
FT DOMAIN 1464 1719
FT DOMAIN 1711 1774
FT DOMAIN 1824 1891
FT NP_BIND 1470 1478
FT BINDING 1493 1493
FT ACT_SITE 1585 1585
FT DOMAIN 1906 1914
FT DOMAIN 868 998
FT REPEAT 868 895
FT REPEAT 896 923
FT REPEAT 924 951
FT REPEAT 952 979
FT REPEAT 980 998
FT DOMAIN 999 1063
FT REPEAT 999 1003
FT REPEAT 1004 1015
FT REPEAT 1016 1027
FT REPEAT 1028 1039
FT REPEAT 1040 1051
FT REPEAT 1052 1063
FT VARSPLIC 437 506
FT VARSPLIC 1433 1439
FT VARSPLIC 1473 1546
FT VARSPLIC 1655 1705
FT VARSPLIC 1790 1790
FT CONFLICT 933 933
FT CONFLICT 963 963
FT CONFLICT 1022 1022
FT CONFLICT 1048 1050
FT CONFLICT 1162 1162
FT CONFLICT 1210 1210
FT CONFLICT 1280 1280
FT MISSING (IN ISOFORM 3A AND ISOFORM 3B).
FT MISSING (IN ISOFORM DEL-1790).
FT V -> M (IN REF. 5).
FT S -> P (IN REF. 3; AAD15922).
FT P -> A (IN REF. 5).
FT KPM -> EAH (IN REF. 5).
FT P -> L (IN REF. 3; AAD15922 AND AAD15923).
FT L -> P (IN REF. 5).
FT E -> D (IN REF. 3; AAD15922 AND

FT CONFLICT 1284 1284 AAD15923).
FT M -> I (IN REF. 3; AAD15922, AAD15923 AND AAD15924).
FT CONFLICT 1300 1300 A -> G (IN REF. 5).
FT CONFLICT 1316 1316 L -> S (IN REF. 5).
FT CONFLICT 1326 1326 T -> S (IN REF. 5).
FT CONFLICT 1478 1478 V -> C (IN REF. 5).
FT CONFLICT 1511 1511 S -> T (IN REF. 5; AAD15922 AND AAD15923).
FT CONFLICT 1563 1563 I -> T (IN REF. 5).
FT CONFLICT 1609 1609 A -> P (IN REF. 5).
FT CONFLICT 1639 1639 G -> R (IN REF. 5).
FT CONFLICT 1639 1640 GT -> D (IN REF. 3; AAD15922, AAD15923
Query Match 8.8%; Score 76.5; DB 1; Length 1914;
Best Local Similarity 18.4%; Pred. No. 22;
Matches 48; Conservative 23; Mismatches 73; Indels 117; Gaps 9;
OY 1 TPVSQTTTAA-----TASVSTKPCPSQPPVPPAAK----- 32
DB 335 TEVLKOTSSSTLQAARVQPEPRAPGLVLSGSGERKRPRATPPTRPGLGSDPV 394
OY 33 -----QCPALEVTPEVEYPLNGTSLSCVACSRFPNFSILYWLGNCS 75
DB 395 VKAANRRITPMGQRDSAPFPKESKPOSOEVENOTVFRCEVSGIRPEVAV----- 447
OY 76 FIEHLPGRLMGSTG--RERGS-----TGTOLCRA-----L 104
DB 448 FLEGTPVRMGESIEYEDAGSHYLCLKARTDSQTSCTASNAQGVSCSWTLQVERL 507
OY 105 VLEQLPALHSTNFCVLYDPQVYORAHVLAQLNAGLRATLP----- 148
DB 508 AVMEVAPSSVSLKCAVIEGDFV-----LQCSVNGTVPRTIWLNGPIQYAKS 559
OY 149 -----TQEALPSSHS 159
DB 560 TCEAGVAELHIDALPEDHGT 580
RESULT 8
CCRS_RAT
ID CCR5_RAT STANDARD: PRT: 374 AA.
AC P34997;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-X-C chemokine receptor type 5 (CXCR-5) (Burkitt's lymphoma
DE receptor 1 homolog) (Neurolymphatic receptor) (NLR).
CN BRLT OR CXCR5
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=93238948; PubMed=8386678;
RA Kouba M., Vanetti M., Wang X., Schaefer M., Hoelle V.;
FT "Cloning of a novel putative G-protein-coupled receptor (NLR) which
FT is expressed in neuronal and lymphatic tissue.";
RL FEBS Lett. 321:173-178(1993).
CC -I- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO B LYMPHOCYTE
CC -I- CHEMOKINE RECEPTOR (BLC) (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: EXPRESSED IN NEURONAL AND LYMPHATIC TISSUE.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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Query Match	8.78;	Score 76;	DB 1;	Length 374;
Best Local Similarity	18.88;	Pred. NO. 3.4;		
Matches 44;	Conservative 33;	Mismatches 61;	Indels 96;	Gaps 11

9	RESULT	505	AA
0	STANDARD;	PRT;	
0	CXAA_MOUSE		
0	KAA_MOUSE		

"Molecular cloning and functional expression of the mouse gap junction gene connexin-57 in human Hela cells.",
J. Biol. Chem. 274:14716-14723(1999).

Query Match	8.7%;	Score 75.5;	DB 1;	Length 505;
Best Local Similarity	23.4%;	Pred. NO. 5.5;		
Matches 29;	Conservative 15;	Mismatches 39;	Indels 41;	Gaps 5;

RESULT	10
CO2_HUMAN	
MO2_HUMAN	
STANDARD;	PRT; 2004 AA

SEQUENCE FROM N.A.
MEDLINE=96376968; PubMed=8782817;

Borrow J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G., Chaganti R.S.K., Clavin C.I., Distche C., Dube I., Erischauf A.M., Hosman D., Mitleman F., Volinia S., Walmoe A.E., Hosman D.E.;
 "The translocation t(8;16)(p11;p13) of acute myeloid leukaemia fuses a putative acetyltransferase to the CREB-binding protein.";
 Nat. Genet. 14:33-41(1996).
 RL Genet. 14:33-41(1996).
 CC -1- FUNCTION: MAY REPRESENT A CHROMATIN-ASSOCIATED ACTIVITYTRANSFERASE.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DISEASE: PARTICIPATES IN A T(8;16)(p11;p13) CHROMOSOMAL TRANSLOCATION THAT PRODUCES A MOZ-CBP CHIMERA OBSERVED IN THE M4/M5 SUBTYPE OF ACUTE MYELOID LEUKEMIA.
 CC -1- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
 CC -1- SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.

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 CC EMBL; U47742; AAC50662.1; .
 DR HSSP; 060631; 4GBQ.
 DR MIM; 601408; .
 DR InterPro; IPR001386; Linker_histone.
 DR InterPro; IPR002717; MOZ_SAS.
 DR InterPro; IPR001965; PHD.
 DR Pfam; PF01853; MOZ_SAS; 1.
 DR Pfam; PF00628; PHD; 2.
 DR SMART; SM00526; H15; 1.
 DR SMART; SM00249; PHD; 2.
 KW Proto-oncogene; Chromosomal translocation; Zinc-finger; Repeat;
 KW Nuclear protein.
 FT ZN_FING 206 256 PHD-TYPE 1.
 FT ZN_FING 259 313 PHD-TYPE 2.
 FT DOMAIN 371 379 POLY-SER.
 FT ZN_FING 538 560 C2HC-TYPE.
 FT DOMAIN 788 801 POLY-GLU.
 FT DOMAIN 989 995 POLY-GLU.
 FT DOMAIN 1019 1026 POLY-ARG.
 FT DOMAIN 1069 1078 POLY-GLU.
 FT DOMAIN 1147 1150 POLY-IVS.
 FT DOMAIN 1221 1242 GLU-RICH.
 FT DOMAIN 1267 1302 GLU-RICH.
 FT DOMAIN 1411 1414 POLY-SER.
 FT DOMAIN 1593 1597 POLY-SER.
 FT DOMAIN 1643 1704 GLN/PRO-RICH.
 FT DOMAIN 1897 1977 MET-RICH.
 FT SITE 1546 1547 BREAKPOINT FOR TRANSLOCATION TO FORM MOZ-CBP.
 FT SEQUENCE 2004 AA; 225054 MW; 9FDBAC3792854BA CRC64;

 Query Match 8.7%; Score 75.5; DB 1; Length 2004;
 Best Local Similarity 24.9%; Pred. No. 29;
 Matches 42; Conservative 17; Mismatches 61; Indels 49; Gaps 7;

 QY 20 PCPSQPPVPAKQCPALE-----VTWPEV-EVPLNGTSLSCVACSRPNFSILYW 70
 Db 1685 POPQPPPPPPPOQPPPLSQCSMNNSFPAPMIMEIPESGS----- 1725

 QY 71 LGNSFTFHLGRLMEGSTREKSTGTQLCKALVLEOLT-----PAL-H 114
 Db 1726 TGNSTIYERIPDGCAGYSOP--SNFSLAK-----LQQLTITMDPHAMPYSHSPAVSY 1780
 QY 115 STNFSCLVDEPQVYVVRHVLVLAQLAGRLPTQGLALPSHSSPQOQ 163
 Db 1781 ATSVSLSTGLAQLAPSHPLAGTPOAQATMPRPVLAFTMTLTLSPLOQ 1829

 RESULT 11
 ILIS_RAT

ILIS_RAT STANDARD: PRT; 416 AA.
 AC P43303;
 DT 01-NOV-1995 (Rel. 32; Created)
 DT 01-NOV-1995 (Rel. 32; Last sequence update)
 DT 01-MAR-2002 (Rel. 41; Last annotation update)
 DE Interleukin-1 receptor, type II precursor (IL-1R-2).
 GN IL1R2 OR IL1RB OR IL-1R2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95035882; PubMed=7524717;
 RA Bristulf J., Gatti S., Malinowsky D., Bjork L., Sundgren A.K., Barfal T.;
 "Interleukin-1 stimulates the expression of type I and type II interleukin-1 receptors in the rat insulinoma cell line Rinn5F; sequencing a rat type II interleukin-1 receptor, cDNA.";
 RL Eur. Cytokine Netw. 5:319-330(1994).
 CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B), AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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 CC EMBL; 222812; CAA80465.1; .
 DR HSSP; P14778; IIRB.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR004077; Intlik_receptorII_pre.
 DR InterPro; IPR004074; Intlikn_receptorII.
 DR Pfam; PF00047; Ig; 3.
 DR PRINTS; PR01539; INTRLEUKN1R2.
 DR PRINTS; PR01536; INTRLEUKN1R2F.
 DR SMART; SM00409; IG; 3.
 KW Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
 KW SIGNAL.
 FT CHAIN 1 13 POTENTIAL.
 FT DOMAIN 14 416 INTERLEUKIN-1 RECEPTOR, TYPE II.
 FT DOMAIN 356 381 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 382 416 POTENTIAL.
 FT DOMAIN 57 127 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 127 127 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 157 226 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 263 345 IG-LIKE C2-TYPE DOMAIN 3.
 FT DISULFD 64 120 BY SIMILARITY.
 FT DISULFD 164 219 BY SIMILARITY.
 FT DISULFD 270 338 BY SIMILARITY.
 FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 416 AA; 46353 MW; 50BFBA48881C5DAE CMC64;

 Query Match 8.6%; Score 74.5; DB 1; Length 416;
 Best Local Similarity 20.3%; Pred. No. 5.4;
 Matches 27; Conservative 21; Mismatches 46; Indels 39; Gaps 4;

 QY 66 SILVWLGNGSTFLE-HLPGRLMEGSTREKSTGTQLCKALVLEOLTPLALHSTNFSCLV 123
 Db 282 TIWMMANSTFISVAIPGRVTEGLIHQYSEDDYVVEVSLFDPVKEDLTDQKCVAT 341
 QY 124 DPEQVYVGRH-----VYLAQALMAGLR-----ATLPPT 149

Db 342 NPNRFSGLHTTVKEVSTFSWGIALAPLSLILVGAIWIRRCRQAGKTYGLTKLPTD 401
QY 150 QEALPSSHSSPQ 162
Db 402 NQDPF---SSPNO 411

RESULT 12
MY15_MOUSE STANDARD: PRT: 3511 AA.
AC 090224: 070395; Q9QWLG6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin XV (Unconventional myosin-15).
GN MYO15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=20021762; PubMed=10552926;
RA Liang Y., Wang A., Belyantseva I.A., Anderson D.W., Probst F.J.,
Barber T.D., Miller W., Touchman J.W., Jin L., Sullivan S.L.,
R. Sellers J.R., Camper S.A., Lloyd R.V., Kachar B., Friedman T.B.,
Fridell R.A.;
RT "Characterization of the human and mouse unconventional myosin XV
genes responsible for hereditary deafness DFNB3 and Shaker 2.";
RL Genomics 61:243-258(1999).
RN [2]
RP SEQUENCE OF 1168-2970 FROM N.A., AND VARIANT SH2 TYR-1779.
RC TISSUE=Embryo;
RX MEDLINE=98267310; PubMed=9603735;
RA Probst F.J., Fridell R.A., Raphael Y., Saunders T.L., Wang A.,
Liang Y., Morell R.J., Touchman J.W., Lyons R.H., Noben-Trauth K.,
Friedman T.B., Camper S.A.;
RT "Correction of deafness in shaker-2 mice by an unconventional myosin
in a BAC transgene.";
RL Science 280:1444-1447(1998).
RN [3]
RP SEQUENCE OF 1237-1823 FROM N.A., AND VARIANT SH2 TYR-1779.
RC STRAIN=C57BL/6;
RX MEDLINE=98369604; PubMed=9703981;
RA Wakabayashi Y., Takahashi Y., Kikkawa Y., Okano H., Mishima Y.,
Ushiki T., Yonekawa H., Komihama R.;
RT "A novel type of myosin encoded by the mouse deafness gene shaker-2.";
RL Biochem. Biophys. Res. Commun. 248:655-659(1998).
CC -I- FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE
ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN INTRACELLULAR MOVEMENTS.
THEIR HIGHLY DIVERGENT TAILS ARE PRESUMED TO BIND TO MEMBRANOUS
COMPARTMENTS, WHICH WOULD BE MOVED RELATIVE TO ACTIN FILAMENTS (BY
SIMILARITY). MAY PLAY A ROLE IN THE FORMATION OR MAINTENANCE OF
THE ACTIN-RICH STRUCTURES OF THE INNER EAR SENSORY HAIR CELLS.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- TISSUE SPECIFICITY: IN THE DEVELOPING INNER EAR. EXPRESSED IN
COCHLEA AND VESTIBULAR APPARATUS. EXPRESSION APPEARS TO BE
RESTRICTED TO COCHLEAR NEUROSENSORY CELLS AND UPPER EPITHELIAL
LAYER OF MACULA SACCULE. ALSO EXPRESSED IN MACULA UTRICULI AND
CRISTAE AMPULLARIS OF THE SEMICIRCULAR CANALS. IN ADULT COCHLEAR
HAIR CELLS, HIGHEST EXPRESSION IN STEREOCILIA AND APICAL BODY.
CC -I- DISEASE: DEFECTS IN MYO15 ARE THE CAUSE OF SHAKER 2 (SH2), A
CONDITION CAUSING DEAFNESS, CIRCLING BEHAVIOR, HEADTOSING AND
HYPERACTIVITY. AUDITORY HAIR CELLS OF AFFECTED ANIMALS HAVE VERY
SHORT STEREOCILIA AND A LONG ACTIN-CONTAINING PROTRUSION AT THEIR
BASAL END.
CC -I- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -I- SIMILARITY: CONTAINS 2 IO DOMAINS.
CC -I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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DR EMBL: AF144095; AAF05904.1; -;
DR EMBL: AF053130; AAC40124.1; -;
DR EMBL: AB014510; BAA36582.1; -;
DR HSSP: P08799; ILVK
DR MGD: MGI:1261811; Myo15.
DR InterPro: IPR000299; Band_4.1.
DR InterPro: IPR000048; IO.
DR InterPro: IPR000857; MYTH4.
DR InterPro: IPR001452; MYTH3.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00612; IO; 2.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF00784; MYTH4; 2.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IO; 2.
DR SMART: SM00242; MYSC; 1.
DR SMART: SM00139; MYTH4; 2.
DR PROSITE: PS50096; SH3; 1.
DR PROSITE: PS50002; SH3; 1.
DR PROSITE: PS00660; BAND_4_1; FALSE_NEG.
DR PROSITE: PS00661; BAND_4_1_2; FALSE_NEG.
DR PROSITE: PS50057; BAND_4_1_3; FALSE_NEG.
KW Myosin; ATP-binding; Actin-binding; Coiled coil; Repeat; SH3 domain;
KW Disease mutation; Deafness.
FT DOMAIN 1 1871 HEAD OR MOTOR DOMAIN.
FT DOMAIN 1872 2013 NECK OR REGULATOR DOMAIN.
FT DOMAIN 2014 3511 TAIL.
FT DOMAIN 1307 1334 COILED COIL (POTENTIAL).
FT DOMAIN 1776 1783 ACTIN-BINDING (POTENTIAL).
FT DOMAIN 1886 1908 IO 1.
FT DOMAIN 1909 1938 IO 2.
FT DOMAIN 2848 2934 SH3.
FT DOMAIN 3187 3424 BAND 4.1-LIKE.
FT NP_BIND 1299 1306 ATP (POTENTIAL).
FT VARIANT 1779 1779 C -> Y (IN SH2).
FT CONFLICT 1330 1331 MISSING (IN REF. 2).
FT CONFLICT 1579 1579 L -> R (IN REF. 3).
FT CONFLICT 1955 1972 MISSING (IN REF. 2).
FT CONFLICT 2077 2077 L -> M (IN REF. 2).
FT CONFLICT 2139 2139 L -> P (IN REF. 2).
FT CONFLICT 2953 2953 V -> A (IN REF. 2).
SQ SEQUENCE 3511 AA; 395533 MW; 38C962F98A2D395B CMC64;

Query Match 8.6%; Score 74.5; DB 1; Length 3511;
Best Local Similarity 24.3%; Pred. No. 73;
Matches 45; Conservative 24; Mismatches 67; Indels 49; Gaps 9;

QY 9 AATAVRSTDPDPPSQ---PVPPAAK--QCPALVTPVEVPPLNLTLSLCY-----A 58
Db 2010 AVVRAAPRLQAPCVTLPLDLINNPMAKFKIRCKEKEPSFGMLTVPLKMLPRLRLEHHAAE 2069
QY 59 CSRPPEHSILYWGNN-----GSFTEH-----LPRLWE--GSTS 90
Db 2070 ISYFK--LILRFMGDHLHNGTOMILGNITVHGGLVEPALRDELQLANOVYRNPNAYN 2127
QY 91 RERGSTGTQCRALVEQLTPALHSTNFCVLDP-----QVYVRHVYLAQLMAGIRAT 145
Db 2128 SKRG-----WLLAACLSGFAPSPDLKFLKLFVSDYGONGFQAVVCHRLQLAMGSGAART 2183
QY 146 LPPTQ 150
Db 2184 FPPTQ 2188

Query Match	Best Local Similarity	8.4%	Score 73.5	DB 1	Length 1172
Matches 35	Conservative 17	Mismatches 54	Indels 37	Gaps 9	
Db	1	TPVQOTTAATASVRSKTDPCSPQPPVPAKQCPALFVTNPEV----	EVPLNGTSLISC	56	
Db	501	SPWNACTYTCAGGIRERKRCVNCSPPEQY-GGKDCYG-DYTEHOMKNKKSCTPDLGCLSNPC	558		
Qy	57	--VACSNFPNFSILYW-----LNGSFIETHLPGRLMEGSGTSRERGSGTGLCKAL	104		
Db	559	FPGAKCNSEPPDGS---WGCSCGPVGLGNGHRCEDL-----DECAVAVTDICFS-	603		
Qy	105	VLEQUTPALHSTN--FSCVLYDP	125		
Db	604	--TNKAPRCVNTNPGFHCLPCP	624		
RESULT 15					
ID	LHR_ECOLI	STANDARD	PRT	1538 AA.	
AC	P30015				
DT	01-APR-1993 (Rel. 25, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Probable ATP-dependent helicase Itr (EC 3.6.1.-) (Large helicase-related protein).				
DE	LHR OR RHLF OR B1653.				
OS	Escherichia coli.				
OC	Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.				
OX	NCBI_Taxid=562;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-K12				
RX	MEDLINE=96032370; PubMed=7559321;				
RA	Reuven N.B., Koonin E.V., Rudd K.E., Deutscher M.P.,				
RT	"The gene for the longest known Escherichia coli protein is a member of helicase superfamily II."				
RL	J. Bacteriol. 177:5393-5400(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-K12 / MG1655;				
RX	MEDLINE=97426617; PubMed=9278503;				
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,				
RT	Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,				
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,				
RT	Mau B., Shao Y.;				
RL	"The complete genome sequence of Escherichia coli K-12."				
RN	Science 277:1453-1474(1997).				
RP	[3]				
RC	SEQUENCE FROM N.A.				
RX	STRAIN-K12				
RA	MEDLINE=97251357; PubMed=9097039;				
RT	Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,				
RA	Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,				
RA	Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,				

RA Mocommura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubramaniam S.,
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA Yamamoto Y., Horikuchi T.,
RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.",
RL DNA Res. 3:363-377(1996).
RN [4]
RP SEQUENCE OF 1-130 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=93094287; PubMed=1460056;
RA Huang S., Deutscher M.P.;
RT "Sequence and transcriptional analysis of the *Escherichia coli* rnt
RT gene encoding RNase T.",
RL J. Biol. Chem. 267:25609-25613(1992).
CC -1- SIMILARITY: WITH OTHER ATP DEPENDENT HELICASES.

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CC
DR EMBL; L01622; AAC37009.1; "-"
DR EMBL; AE000260; AAC74725.1; "-"
DR EMBL; D90809; BAA15419.1; "-"
DR PIR; B45065; B45065.
DR Ecogene; EG11548; lnt.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD. 1.
DR Pfam; PF00271; helicase_C. 1.
DR SMART; SM00487; DEXDC. 1.
DR SMART; SM00490; HELIC_C. 1.
DR HydroLase; Helicase; ATP-binding; Complete proteome.
FT NP_BIND 51 58
FT SITE 179 182
FT DEVI BOX.
FT ATP (BY SIMILARITY).
SQ SEQUENCE 1538 AA; 169380 MW; 563172B5FE3D826E CRC64;

FEATURES	source	Location/Qualifiers
BASE COUNT	97 a 171 c 136 g 88 t	
ORIGIN	/organism="Homo sapiens" /db_xref="taxon:9606"	
Query Match	100.0%	Score 492; DB 6; Length 492;
Best Local Similarity	100.0%	Pred. No. 3.2e-102;
Matches 492; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1	aacactgtctgcacaaccacccacacagctgcgcacttgctcgtatgaagaacaaagacc 60
DB	1	ACACTGTCTGCAGACACCCACAGCTGCCTCTGTTAGAAAGCAAGAGACCCC 60
OY	61	tgccccctccacagcccccagtgctccacagcgtaaagcagtgctccagcattgaaatgacc 120
DB	61	TGCCCTCTCCAGACCCCAAGTGTTCACAGAGCTAAGACAGTGTCCAGATTTGGAAGTGACC 120
OY	121	tgccagagagtggaagtgccactgaatggaacgctgaagcttaccctgtgtgctgcagc 180
DB	121	TGGCCAGAGAGTGGAAAGTGCCTAGATGGAACGCTGAGAGCTTATCCTGTGTGGCTGCAGAC 180
OY	181	cgcttcccccaattcagcatctctctactgcgtgcgtggcgaatgfttccttatagaccctc 240
DB	181	CGCTTCCCCCACTTACGATCTCTTACTGTGGCTGGGCAATGGTTCCTTCAATTGAGCACCTC 240
OY	241	ccagagccgactgtggagagggagacacagccggagagctgagagacagatgacgacgtg 300
DB	241	CCAGGCCGACGCTGGGAGAGGGAGACACGACGGGAACGTGGAGACACAGGTACGCAGCTG 300
OY	301	tgcaagagcctgtgtgtctgtgagcagctgacccctgcctgcgacagacacaacttctctgt 360
DB	301	TGCAAGAGCCTGTGTGCTGTGAGCAGCTGACCCCTGCCTGCACAGCACCAACTTCTCTGT 360
OY	361	gtgcctcgtggagaccctggaacaagtttccagagtgacgtgcgtctgtgcccagctcggagct 420
DB	361	GTGCTCTGTGACCTGTGAACAGGTGTCCAGGCTCACGCTGCTGTGCCCCAGCTGTGGGCT 420
OY	421	ggagctgagggacaactctgccccccacccaagaagagccctgcgcccctcagccacagcagctca 480
DB	421	GGGCTGAGGGGCAACTTGTGCCCCCCACCAAGAAGCCCTGTGCTTCCAGCCACAGCAGTCCA 480
OY	481	cagcagcagaggt 492
DB	481	CAGCAGCAGAGGT 492
RESULT 2		
LOCUS	AB019504	585 bp mRNA linear PRI 31-MAR-1999
DEFINITION	Homo sapiens mRNA for interleukin-18 binding protein, complete cds.	
ACCESSION	AB019504	
VERSION	AB019504.1	GI:4586394
KEYWORDS	interleukin-18 binding protein.	
SOURCE	Homo sapiens (isolate:white) male liver cDNA to mRNA.	
ORGANISM	Homo sapiens	
REFERENCE	Eumayorita; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	1 (sites)	
TITLE	Cloning and expression of interleukin-18 binding protein	
JOURNAL	FEBS Lett. 445 (2-3), 338-342 (1999)	
MEDLINE	99192308	
REFERENCE	2 (bases 1 to 585)	

AUTHORS Aizawa, Y.
 TITLE Direct Submission
 JOURNAL Submitted (04-NOV-1998) Yasushi Aizawa, Hayashibara Biochemical Laboratories, Inc., Fujisaki Institute; 675-1, Fujisaki, Okayama, Okayama 702-8006, Japan (E-mail: fujisaki@hayashibara.co.jp, Tel: 81-86-276-3141, Fax: 81-86-276-6885)
 COMMENT Sequence updated (30-Nov-1998).
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 Best Local Similarity 100.0%; Pred. No. 3.1e-102;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 aaacctgtctgcagagacacccacacagctgcctacatgctctgaagtagaacacaaagagccccc 60
 Db 91 AACCTGTCTGCAGACCCACACACACTGTCACCTGCTCAGTAGAAGACAAAGAGACCCC 150
 QY 61 tgcacctccacagcccccaagtgttcccaagactaaagcagtgctcagacatltggaatgacc 120
 Db 151 TGCACCTCCACACCCCCCAAGTGTCCACAGAGCTAAGCAAGTGTCCAGCATGTGAATGAC 210
 QY 121 tggcagagatggaagtgtcactgaatggaacgtctgaagctatcctgtgtggtctgacg 180
 Db 211 TGGCAGAGAGTGAAGTGCACATGAATGGAACGTGAGCTATCTGTGTGCTGCAGC 270
 QY 181 cgtctccccaacttaagatcctctactacgtgcgtgggcaatggtctctatctgagacctc 240
 Db 271 CGCTTCCCAACTTAAGCATCTCTACGTGGCGTGGCAATGTTCTTAAATGAGCACCTC 330
 QY 241 ccagagccagacttgggaagggagacacagcccggaagcttgggaagacagatgacgacgtg 300
 Db 331 CCAGGCCCACTTGGGAGGGGAGACACACCGGGAACGTGGAGACACAGTACGACGTG 390
 QY 301 tgcagaagccttggctgtgagcagcttgacccctgacctgcctgcacagacacaaactctctgt 360
 Db 391 TGCAGAGCCTTGGTGTCTGCTGAGAGCACTGACCCCTGCCTGCACAGACCAACACTTCCTGT 450
 QY 361 gtgtcgtgtggaacctgaaagagtggttccaagtgtaagtcagtcgctcgtggccagcttggct 420
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 QY 421 gggctggaaggcaactctgccccccacccaagaagccctgcgctccagccacagacagttcca 480
 Db 511 GGGCTGAGGGCAACTCTTGCCCCCACCACCAAGAGGCCCTGCCTCCAGCCACAGCAGTGTCA 570
 QY 481 cagcagcagaggt 492
 Db 571 CAGCAGCAGGGT 582

LOCUS E58840 744 bp DNA linear PAT 31-JAN-2002
DEFINITION Interleukin 18 binding protein.
ACCESSION E58840
VERSION E58840.1 GI:18629913
KEYWORDS JP 2000210087-A/6.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS Torikoshi, K., Tanai, M. and Kurimoto, M.
TITLE Interleukin 18 binding protein
JOURNAL Patent: JP 2000210087-A 6 02-AUG-2000;
HAYASHIBARA BIOCHEM LAB INC
COMMENT OS Homo sapiens (human)
PN JP 2000210087-A/6
PD 02-AUG-2000
PE 28-MAY-1999 JP 1999149498
PR
PI RAKUJI TORIKOSHI, MADOKA TANAI, MASASHI KURIMOTO
C12N15/09, A61K31/00, A61K38/00, A61K39/395, C07K14/47, C07K14/715, PC
C07K16/18//
PC C12P21/08, C12N15/00, A61K37/02
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FH Key Location/Qualifiers
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FEATURES
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BASE COUNT 156 a 249 c 200 g 139 t
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Best Local Similarity 100.0%; Pred. No. 3.1e-102;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 160 AACCTGTCTCGACACACACAGCTGCCTCAGTTAGAGCAAAAGGACCCC 219
QY 61 tggccctcccaagccccaagtgltcccaagcagctaaagcagttcccaagcattggaagtgcac 120
DB 220 TGGCCCTCCACAGCCCAAGTGTCCAGCAGCTAAGCAGTGTCCAGCATTTGGAAGTGACC 279
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QY 181 cgcttccccaacttaagcattctctactgtgtgtggcgaatggttctcttaattgagcacc 240
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QY 241 ccaagccgaactgtggagagggagacacacgcggaacgtggagagcaggtacgcagctg 300
DB 400 CCAGCGCGACTGTGGAGGGAGACACACACCGGGAACGTGGAGACACAGGTACGCAAGCTG 459
QY 301 tgcgaagccttggtgtgtgagcagctgacccctgcccctgacagcaaccaattctctgt 360
DB 460 TGCAGGCGCTTGTGTGTGAGAGCTGAGCCCTGACAGCACTTCTCTCTGT 519
QY 361 gtgtctcgttgagaccctggaagaggtgtccaggttcaagtgctgtctgtgcccagcttgaggt 420
DB 520 GTGTCTGTGTGACCTGAACAGGTGTGTCAGCGTCAAGTGTCTGTGCTGAGCTGTGGCT 579
QY 421 gggcttgaaggcaaccttgcccccaaccaagaagccctgcctccagcaagcaagcaatcca 480
DB 580 GGGCTGAGGGCAACCTTGCCCCCAACCAAGAAAGCCCTCCCTCCAGCCACACAGCACTCCA 639
QY 481 cagcagcagaggt 492
DB 640 CAGCAGCAGAGGT 651

RESULT 4
LOCUS AX005900 1348 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 1 from Patent WO9909063.
ACCESSION AX005900
VERSION AX005900.1 GI:9928886
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1348)
AUTHORS Rubinstein, M. and Kim, S.H.
TITLE Interleukin-18 binding proteins, their preparation and use
JOURNAL Patent: WO 9909063-A 1 25-FEB-1999;
RUBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)
FEATURES
source 1..1348
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BASE COUNT 304 a 449 c 292 g 303 t
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Query Match 100.0%; Score 492; DB 6; Length 1348;
Best Local Similarity 100.0%; Pred. No. 3e-102;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 210 TGGCCCTCCACAGCCCAAGTGTCCAGCAGCTAAGCAGTGTCCAGCATTTGGAAGTGACC 269
QY 121 tggcagaagtggaagtgcacactgaaatggaacgctgagcttaacctgtgtggccttgacgc 180
DB 270 TGGCCAGAGTGGAAAGTGCACCTGAATGGAACGCTTATCTGTGTGGCTGACGC 329
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QY 361 gtgtcttgaagccttaaacaggtgtgccagcgtcagctgtctgtgcccagcttgaggt 420
DB 510 GTGTCTGTGTGACCTGAACAGGTGTGTCAGCGTCAAGTGTCTGTGCTGAGCTGTGGCT 569
QY 421 gggcttgaaggcaaccttgcccccaaccaagaagccctgcctccagcaagcaagcaatcca 480
DB 570 GGGCTGAGGGCAACCTTGCCCCCAACCAAGAAAGCCCTGCGCTCCAGCCACAGCACTCCA 629
QY 481 cagcagcagaggt 492
DB 630 CAGCAGCAGAGGT 641
RESULT 5
LOCUS AF110799 1348 bp mRNA linear PRI 03-MAR-1999
DEFINITION Homo sapiens interleukin-18 binding protein a precursor (1L18P)
ACCESSION AF110799

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VERSION      AF110799.1  GI:4324927
KEYWORDS
SOURCE       human
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
              1 (bases 1 to 1348)
              Novick,D., Kim,S.H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A. and
              Rubinstein,M.
TITLE        Interleukin-18 binding protein: a novel modulator of the Th1
              cytokine response
JOURNAL      Immunity 10 (1), 127-136 (1999)
MEDLINE      99146382
REFERENCE    2 (bases 1 to 1348)
AUTHORS      Novick,D., Kim,S.H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A.
              and Rubinstein,M.
TITLE        Direct Submission
JOURNAL      Submitted (04-DEC-1998) Molecular Genetics, Weizmann Institute of
              Science, P.O. Box 26, Rehovot 76100, Israel
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BASE COUNT   304 a 449 c 292 g 303 t
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Query Match      100.0%; Score 492; DB 9; Length 1348;
Best Local Similarity 100.0%; Pred. No. 3e-102;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 361 gtgcctgtgacctgaacaggtgtgcagcgcgtcaagtcgtctcgtgcccagctcggct 420
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QY 421 gggctgaagggaaccttgcacccacccaagaagccctgcctcagcagcagtcaca 480
DB 570 GGGCTGAGGGCAACCTTGCCCCCACCACCAAGAGCCCTCCCTCCAGCAGCAGATCCA 629
QY 481 cagcagcaggt 492
DB 630 CAGCAGCAGGCT 641
RESULT 6
LOCUS      AF122906 1355 bp mRNA linear PRI 28-JUN-1999
DEFINITION Homo sapiens MC51L-53L-54L homolog mRNA, complete cds.
ACCESSION AF122906
VERSION    AF122906.1 GI:5231015
KEYWORDS
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 1355)
AUTHORS    Xiang,Y. and Moss,B.
TITLE      Identification of human and mouse homologs of the MC51L-53L-54L
            family of secreted glycoproteins encoded by the Mollusum
            contagiosum poxvirus
JOURNAL    Virology 257 (2), 297-302 (1999)
MEDLINE    99263157
PUBMED     10329540
REFERENCE  2 (bases 1 to 1355)
AUTHORS    Xiang,Y. and Moss,B.
TITLE      Direct Submission
JOURNAL    Submitted (25-JAN-1999) NIAID/LVD, NIH, 9000 Rockville Pike,
            Bethesda, MD 20892, USA
FEATURES
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BASE COUNT   293 a 455 c 298 g 309 t
ORIGIN
Query Match      100.0%; Score 492; DB 9; Length 1355;
Best Local Similarity 100.0%; Pred. No. 3e-102;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 649 CAGCAGCAGGCT 660

RESULT 7

AF110801

LOCUS

3630 bp mRNA linear PRI 03-MAR-1999

DEFINITION

Homo sapiens interleukin-18 binding protein c precursor (IL18BP)

ACCESSION

AF110801

VERSION

AF110801.1 GI:4324931

KEYWORDS

.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

TITLE

Novick, D., Kim, S.H., Fantuzzi, G., Reznikov, L.L., Dinarello, C.A. and

JOURNAL

Interleukin-18 binding protein: a novel modulator of the Th1

MEDLINE

cytokine response

REFERENCE

Immunology 10 (1), 127-136 (1999)

AUTHORS

2 (bases 1 to 3630)

TITLE

Novick, D., Kim, S.H., Fantuzzi, G., Reznikov, L.L., Dinarello, C.A.

JOURNAL

Direct Submission

MEDLINE

Submitted (04-DEC-1998) Molecular Genetics, Weizmann Institute of

AUTHORS

Science, P.O. Box 26, Rehovot 76100, Israel

FEATURES

Location/Qualifiers

SOURCE

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REFERENCE

/db_xref="taxon:9606"

AUTHORS

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JOURNAL

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MEDLINE

1..3630

AUTHORS

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JOURNAL

929..1522

MEDLINE

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AUTHORS

/codon_start=1

JOURNAL

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MEDLINE

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AUTHORS

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JOURNAL

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MEDLINE

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 BASE COUNT 834 a 1022 c 995 g 779 t
 ORIGIN

Query Match 85.0%; Score 418.2; DB 9; Length 3630;
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 Matches 420; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 acactgtctcgaagaccaccagcagctgacagctgctcagcttagaagacaaagacc 60
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 Db 1373 GTGCTGTGAGCCCTGAACAGGTTGTCCAGCGTACGTCGTCCTGGCCAGCTCTGGGCT 1432
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 Db 1433 AGG 1435

RESULT 8

AX005904

LOCUS

AX005904

DEFINITION

Sequence 5 from Patent WO9909063.

ACCESSION

AX005904

VERSION

AX005904.1 GI:9228888

KEYWORDS

.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

JOURNAL

Interleukin-18 binding proteins, their preparation and use

MEDLINE

Patent: WO 9909063-A 5 25-FEB-1999;

AUTHORS

ROBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)

JOURNAL

Location/Qualifiers

FEATURES

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ORGANISM

/organism="Homo sapiens"

REFERENCE

/db_xref="taxon:9606"

AUTHORS

BASE COUNT 1538 a 2025 c 1981 g 1519 t

JOURNAL

ORIGIN

Query Match

85.0%; Score 418.2; DB 6; Length 7063;

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Db 493 CCAGGCCGACTGTGGAGGGAGCACCAGCGGAACTGGAGACAGCCTGGGCTGAG 552
QY 301 tggca 305
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Db 553 GGCAA 557

RESULT 11
AF215907 1726 bp mRNA linear PRI 24-MAR-2000
LOCUS AF215907
DEFINITION Homo sapiens interleukin-18 binding protein d (IL18BP) mRNA,
complete cds.
ACCESSION AF215907
VERSION AF215907.2 GI:7327285
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1726)
Kim,S.H., Eisenstein,M., Reznikov,L., Fantuzzi,G., Novick,D.,
Rubinstein,M. and Dinarello,C.A.
Structural requirements of six naturally occurring isoforms of the
IL-18 binding protein to inhibit IL-18
Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1190-1195 (2000)
MEDLINE 20122593
PUBMED 10655506
REFERENCE 2 (bases 1 to 1726)
Kim,S.H., Novick,D., Dinarello,C.A. and Rubinstein,M.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1999) Molecular Genetics, Weizmann Institute of
Science, POBox 26, Rehovot 76100, Israel
3 (bases 1 to 1726)
Kim,S.H., Novick,D., Dinarello,C.A. and Rubinstein,M.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2000) Molecular Genetics, Weizmann Institute of
Science, POBox 26, Rehovot 76100, Israel
REMARK Sequence update by submitter
COMMENT On Mar 24, 2000 this sequence version replaced gi:6934281.
FEATURES
source location/Qualifiers
1..1726
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q13"
/cell_line="Jurkat"
/cell_type="T cell"
1..1726
/gene="IL18BP"
162..647
/gene="IL18BP"
/note="IL18BP"
/note="inactive splice variant"
/codon_start=1
/product="interleukin-18 binding protein d"
/protein_id="AAF31697.1"
/db_xref="GI:6934282"
/translation="MRHNTPLSPMLLLCAHYVTLVRAFPVSQTTTAATASVRS
TKDPCSPVPVPAKQCPALFVWPEVPLNGTLTSCVACSRRPNSILYWGNGSFI
EHLPGRLMGSTSRERGSTGMAEGLNAPRPSPALPOOSTAAGLRLSTGPAAAO
P"

BASE COUNT 407 a 535 c 412 g 369 t 3 others
ORIGIN

Query Match 59.1%; Score 290.6; DB 9; Length 1726;
Best Local Similarity 97.0%; Pred. No. 2.7e-56;
Matches 296; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 acactgtctgcagagaccacacagctgcccactgctccagttaagaacaaagacccc 60
|||||
Db 246 ACACCTGTCTGCGAGACACACACAGCTGCCACTGCTCTCAGTAGAAGACACAAAGACCCC 305
QY 61 tgcctccccaagcccccaagtgttcccaagcagtaagtgatccagattggaaatgacc 120
|||||
Db 306 TGCCCTTCCAGCCCCAGTAGTTCAGCAGACGTAAAGCAGTGTCCAGATTGGAAGTGACC 365
QY 121 tggcagaaggttggagatgccaactgaaatgtaacgtgtgattatctgtgtgacctgacc 180
|||||
Db 366 TGGCAGAGGTGGAGAGTGCACCTGAATGAAACGCTGAGCTTATCTGTGGCCTGCAGC 425
QY 181 cgttcccccaactcagcatcctctactgctggtggcaatggttcctcattgagcacc 240
|||||
Db 426 CGGTTCCCAACTTCAGCATCTCTACTGGTGGCAATGTTCTTCATTGAGCACCCTC 485
QY 241 ccagggccgaactgtggagggagagcaccgaggaacgttggagacaggtacgcagctg 300
|||||
Db 486 CCAGGCCGACTGTGGAGGGAGCACCAGCGGAACTGGAGACAGCCTGGGCTGAG 545
QY 301 tggca 305
|||||
Db 546 GGCAA 550

RESULT 12
AF154569 626 bp mRNA linear ROD 28-MAY-2000
LOCUS AF154569
DEFINITION Rattus norvegicus interleukin 18 binding protein (IL18BP) mRNA,
complete cds.
ACCESSION AF154569
VERSION AF154569.1 GI:8099343
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 626)
Im,S.H., Venkatesh,N., Barchan,D., Souroujon,M.C. and Fuchs,S.
Cloning and characterization of rat IL-18 binding protein
JOURNAL Unpublished
2 (bases 1 to 626)
Im,S.H., Venkatesh,N., Barchan,D., Souroujon,M.C. and Fuchs,S.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-1999) Immunology, Weizmann Institute of Science,
Herzl, Rehovot 76100, Israel
FEATURES
source location/Qualifiers
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/organism="Rattus norvegicus"
/strain="Lewis"
/db_xref="taxon:10116"
1..626
/gene="IL18BP"
11..592
/gene="IL18BP"
/note="IL18BP; IL18 soluble receptor and antagonist"
/codon_start=1
/product="interleukin 18 binding protein"
/protein_id="AAF72102.1"
/db_xref="GI:8099344"
/translation="MRHGCADPSPFWWVLLYVHYILARATSAFLTTATYVLRSSK
DPCSSSPAVPTKQYPTLDVIMPEKEVPLNGTLTSCVACSRRPNSILYWGNGSFI
EHLPGRLMGSTSRERGNASTWMLRALVLEELSPSLSTNFCLFVDPQVAVQYHVL
AQLMDLKTAPSPSOETLLSHSGPSPGAPCAP"

BASE COUNT 141 a 205 c 154 g 126 t
ORIGIN

Query Match 56.5%; Score 277.8; DB 10; Length 626;
Best Local Similarity 78.5%; Pred. No. 2.4e-53;
Matches 346; Conservative 0; Mismatches 92; Indels 3; Gaps 1;

Query Match	Best Local Similarity	78.0%	Score 272.2	DB 10	Length 873
Matches 341	Conservative	0	Mismatches 93	Indels	Gaps 1
sig_peptide	85..162	/gene="IL18BP"			
mat_peptide	163..657	/gene="IL18BP"			
		/product="Interleukin-18 binding protein d"			
BASE COUNT	203 a	259 c	201 g	210 t	
ORIGIN					
Query Match	Best Local Similarity	78.0% <td>Score 272.2</td> <td>DB 10</td> <td>Length 873</td>	Score 272.2	DB 10	Length 873
Matches 341	Conservative	0	Mismatches 93	Indels	Gaps 1
22	aagctgcacactgctcctcagttagaagacacaaagacccctgcgcctccacagccccaagt	81			
178	ACAACCTGGCCACCTGTTTACTGGAAGCTCAAAAGACCCATGCTCTTCTGGTCTCCACCA	237			
82	ttccagcagacgaagcagctgtccagcatttgaagtgacacttgccagaggtggaagtcca	141			
238	GTCCCAA---CTAACAGTACCCAGACTGATGTGATTTGGCCAGAAAAAGAAAGTGCA	294			
142	ctgaatgaaagctgtagcttatactctgtgtgacctgacgcgccttcccaactgaagc	201			
295	CTGAATGGAACCTGACCTTGCTCTGTACTGCTCCCTCCACGCCCTTCCCTACTTACGATC	354			
202	ctctactgcttgaggaaatgattcctcttaattgaagcaccctccagagcgacacttggaagag	261			
335	CTCTACTGGCTGGGCAATGTTCTTCTTAATTGAGCACTCCAGAGCCGGCTGAAGAGAGGC	414			
262	agcaccagccgggaagctgtggagacacaggtacgcagctgtgcaagagccttggctggag	321			
415	CACACAAGTCGGGACACAGAGACACAGCACTGGCTGCACAGAGGCTTGTTGCTGGAA	474			
322	cagctgacccctgcgcctgcacagcaccacattctcttctgtgcctgtgagccctggaacag	381			
475	GAACTGAGCCCCACCTACGAAGTACCAACTTCTCTTGTGTGTGTGATCTTGACAA	534			
382	gtttgcacgcgtcactgtctcgtgcccaagctcttgagcttgagcttgaaggaacacttggc	441			
535	GTGGCCGAGTATCAATCATATTCTGTGGCCAGCTCGTGAGTGGGTGAAGACAGCTCCGCC	594			
442	cccaccacaagaagccct	458			
595	CCTTCTCAAGAAACCT	611			
RESULT 14					
LOCUS	BC018332	1310 bp	mRNA	linear	ROD 06-DEC-2001
DEFINITION	Mus musculus, interferon gamma inducing factor binding protein,				
ACCESSION	BC018332				
VERSION	BC018332.1				
KEYWORDS	MGC.				
SOURCE	house mouse.				
ORGANISM	Mus musculus.				
REFERENCE	Eukarya;ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.				
TITLE	1 (bases 1 to 1310)				
JOURNAL	Submitted (03-DEC-2001) National Institutes of Health, Mammalian				
	Gene Collection (MGC), Cancer Genomics Office, National Cancer				
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,				
	USA				
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov				
COMMENT	Contact: MGC help desk				
	Email: cgapbs-remail.nih.gov				
	Tissue Procurement: Gilbert Smith, Ph.D.				
	cDNA Library Preparation: Life Technologies, Inc.				

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalobebcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Huijck, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRK Plate: 30 Row: 1 Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, similarity but not identity to protein.

FEATURES

source

1. 1310
/organism="Mus musculus"
/db_xref="LocusID:16068"
/db_xref="taxon:10090"
/clone="MGC:25760 IMAGE:4007411"
/tissue_type="Mammary tumor metastasized to lung.
MMTV-LTR/Mnt1 model. Expression driven by an MMTV-LTR
enhancer."
/clone_lib="NCI CGAP_Lu30"
/lab_host="DH10B"
/note="Vector: pCMV-Sport6"
62..643
/codon_start=1
/product="Interferon gamma inducing factor binding
protein"
/protein_id="AAH18332.1"
/db_xref="GI:17390776"
/translation="MTMRHCMTAGPSSMWVLLVYHVIARATSAPOTTATVLTGSSK
DPCSSSPAVPTKQYPALDVIWPERKVPNGTLTSCSTACSRPFSILYWLNGSFI
EHIPLRGKHTSRHRNTSTWLHRLVLELSPTRSTNFSCLFVDPQVADYHILL
AQLMDGLKTAIPPSQETLSHSPVSAGPVA"
BASE COUNT 334 a 369 c 273 g 334 t
ORIGIN

CDS

Query Match 55.3%; Score 272.2; DB 10; Length 1310;
Best Local Similarity 78.0%; Pred. No. 4.3e-52;
Matches 341; Conservative 0; Mismatches 93; Indels 3; Gaps 1;
ORIGIN
22 acaagtcgcaactgctcagcttagaagacaaagaccctcctccagcccaagtg 81
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
161 ACAAGTCGCACTGCTTAACTGGAAGCTCAAAAGACCCATGCTCTGTCAGCA 220
82 ttccagcagcctaagcagtgctcgaagtggaagtgaccctggcccaagtggaagtgca 141
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
221 GTCCCAA---CTAAGCAGTACCCAGACAGCTGAGTGTGTTGGCAGAAAAAGAGTGCCA 277
142 ctgaatggaagcgtgactatcctgtgtgctgctgcaagcgcctcccaactcaagc 201
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
278 CTGAATGGAAGCTGTGACCTTGCTGCTGACTGCTGACAGCGCTCCCTCACTTCAAGATC 337
202 cctcactgctgggcaatggttcctcactatgagaccctcccaagccgaactgtggaaggg 261
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
338 CTCTACTGGCTGGCAATGTTCTTCATTGAGTACCTCCAGCGCGGTGAAGAGAGGC 397
262 agcacagccgggaagcgtgggaagcacaggttacagcagctgtgcaagccgttggtggaag 321
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
398 CACACAAGTCGCGAGCAGACAGAACACAGACACTGGCTGCACAGGGCCTTGGTGTGAA 457
322 cagctgaaccctgaccctgacacagcaactctcctgtgtgtcgtggaaccttgagag 381
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
458 GAAGTGAAGCCCGACCTACGAGATGACCACTTCTGTTTGTGTTGATCTCTGGACAA 517
382 gtgtgtcagcgttactgtctcctggccagcctgtggtcgtggtcgtggaagcaacttgccc 441
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
518 GTGGCCAGTATCATATTCCTGCGCCAGCTCTGGAGTGGGTTGGAAGACAGCTCCGCC 577

QY 442 cccacccaagaagccct 458
111 111 111 111 111
Db 578 CCTTCTCAAGAAACCT 594

RESULT 15

AF122907 1422 bp mRNA linear ROD 28-JUN-1999
LOCUS AF122907
DEFINITION Mus musculus MC51L-53L-54L homolog mRNA, complete cds.
ACCESSION AF122907
VERSION AF122907.1 GI:5231017

KEYWORDS

house mouse.
Mus musculus.

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 1422)
Xiang, Y. and Moss, B.
Identification of human and mouse homologs of the MC51L-53L-54L
family of secreted glycoproteins encoded by the Molluscum

TITLE

contagiosum poxvirus
Virology 257 (2), 297-302 (1999)

JOURNAL

MEDLINE
99263157
PUBMED
10329540

REFERENCE

2 (bases 1 to 1422)
Xiang, Y. and Moss, B.
Direct Submission
Submitted (25-JAN-1999) NIAID/LVD, NIH, 9000 Rockville Pike,
Bethesda, MD 20892, USA

TITLE

JOURNAL

FEATURES

source

1. 1422
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="skin"
/note="similar to Molluscum Contagiosum Poxvirus family of
secreted glycoproteins"
/codon_start=1
/product="MC51L-53L-54L homolog"
/protein_id="A4D41052.1"
/db_xref="GI:5231018"
/translation="MTMRHCMTAGPSSMWVLLVYHVIARATSAPOTTATVLTGSSK
DPCSSSPAVPTKQYPALDVIWPERKVPNGTLTSCSTACSRPFSILYWLNGSFI
EHIPLRGKHTSRHRNTSTWLHRLVLELSPTRSTNFSCLFVDPQVADYHILL
AQLMDGLKTAIPPSQETLSHSPVSAGPVA"
BASE COUNT 358 a 402 c 306 g 356 t
ORIGIN

CDS

Query Match 55.0%; Score 270.6; DB 10; Length 1422;
Best Local Similarity 77.8%; Pred. No. 9.9e-52;
Matches 340; Conservative 0; Mismatches 94; Indels 3; Gaps 1;
ORIGIN
22 acaagtcgcaactgctcagcttagaagacaaagaccctcctccagcccaagtg 81
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
251 ACAAGTCGCACTGCTTAACTGGAAGCTCAAAAGACCCATGCTCTGTCAGCA 310
82 ttccagcagcctaagcagtgctcgaagtggaagtgaccctggcccaagtggaagtgca 141
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
311 GTCCCAA---CTAAGCAGTACCCAGACAGCTGAGTGTGTTGGCAGAAAAAGAGTGCCA 367
142 ctgaatggaagcgtgactatcctgtgtgctgctgcaagcgcctcccaactcaagc 201
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
368 CTGAATGGAAGCTGTGACCTTGCTGCTGACTGCTGACAGCGCTCCCTCACTTCAAGATC 427
202 cctcactgctgggcaatggttcctcactatgagaccctcccaagccgaactgtggaaggg 261
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
428 CTCTACTGGCTGGCAATGTTCTTCATTGAGTACCTCCAGCGCGGTGAAGAGAGGC 487
262 agcacagccgggaagcgtgggaagcacaggttacagcagctgtgcaagccgttggtggaag 321
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
488 CACACAAGTCGCGAGCAGACAGAACACAGACACTGGCTGCACAGGGCCTTGGTGTGAA 547

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 21:48:24 ; Search time 203.01 Seconds

(without alignments)
4160.987 Million cell updates/sec

Title: US-09-786-130-32

Perfect score: 492

Sequence: 1 acaccgtctccgcagaccac.....gcagtcacacgcagcaggt 492

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq_032802.*
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2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*
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23: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	492	100.0	492	21	AAAI1002 Human mature inter
2	492	100.0	744	21	AAAI1007 Human interleukin
3	492	100.0	1348	20	AAAX24749 Human interleukin
4	492	100.0	1356	21	AAAX27384 Human IGFAM-4 immu
5	418.2	85.0	7063	20	AAAX24751 Human interleukin
6	411	83.5	411	21	AAAI1004 Human IL-18 bindin
7	290.6	59.1	1360	20	AAAX24752 Human interleukin
8	269	54.7	495	21	AAAI1003 Mouse mature inter
9	269	54.7	847	21	AAAI1011 Mouse interleukin

10	235.2	47.8	351	21	AAAI1008 Mouse IL-18 bindin
11	197.8	40.2	495	21	AAAX3451 Mouse secreted exp
12	187.6	38.1	7812	20	AAAX24753 Human interleukin
13	152	30.9	6741	23	AAAX70037 DNA encoding novel
14	152	30.9	6741	23	AAAX70037 DNA encoding novel
15	145	29.5	1038	20	AAAX24750 Human interleukin
16	141	28.7	234	21	AAAI1006 Human IL-18 bindin
17	73	14.8	315	20	AAAX51494 Human secreted pro
18	69.6	14.1	234	20	AAAX13394 Human secreted pro
19	57	11.6	216	21	AAAI1005 Human IL-18 bindin
20	52.2	10.6	253	21	AAAI1010 Mouse IL-18 bindin
21	41.2	8.4	38734	20	AAAX32020 Human METHI relate
22	41.2	8.4	38734	22	AAAC90077 AL021529 cDNA clon
23	41	8.3	4352	22	AAI58667 Human polynucleoti
24	41	8.3	4377	22	AAI60453 Human polynucleoti
25	38.8	7.9	336	21	AAAI1009 Mouse IL-18 bindin
26	38.8	7.9	17612	19	AAAX23494 pseudomonas xpc, O
27	38.8	7.9	17612	21	AAAI3905 pseudomonas alcali
28	38.8	7.9	17612	22	AAAX30870 pseudomonas alcali
29	38.8	7.9	17612	24	AAAD2882 pseudomonas alcali
30	38.2	7.8	44377	18	AAAT78508 platenolide syntha
31	38.2	7.8	44377	18	AAI80414 platenolide syntha
32	36.8	7.5	376	22	AAAX5188 Human immune/haema
33	36.8	7.5	612	20	AAAX42103 Human endometrium
34	36.8	7.5	2966	22	AAAX94804 Human full-length
35	36.6	7.4	609	22	AAAI6023 Fibroblast growth
36	36.6	7.4	8933	23	AAAI17516 Drosophila melanog
37	36.4	7.4	1125	23	AAAS82236 DNA encoding novel
38	36.4	7.4	2454	23	AAAT73797 DNA encoding novel
39	36.2	7.4	1248	21	AAAT87286 S. venezuelae deso
40	36.2	7.4	12441	21	AAAZ87284 S. venezuelae deso
41	36.2	7.4	13613	21	AAAZ87319 Human nervous syst
42	36	7.3	4241	22	AAAI17545 Human nervous syst
43	36	7.3	4241	22	AAAI17546 Human nervous syst
44	35.8	7.3	999	21	AAAX6596 M. smegmatis aryla
45	35.6	7.2	11820	19	AAAI18130 Human chromosome 1

ALIGNMENTS

RESULT 1	
AAAI1002	
ID	AAAI1002 standard; DNA; 492 BP.
XX	AAAI1002;
AC	28-JUL-2000 (first entry)
XX	
DT	Human mature interleukin 18 binding protein coding sequence.
DE	
XX	Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW	regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW	autoimmune disease; ss.
OS	Homo sapiens.
XX	
PN	WO200012555-A1.
XX	
PD	09-MAR-2000.
XX	
PF	18-NOV-1998; 98WO-JP05186.
XX	
PR	01-SEP-1998; 98JP-0247588.
PR	18-NOV-1998; 98JP-0327914.
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI	Torigoe K, Tanial M, Kurimoto M;
XX	
DR	WPI: 2000-237850/20.
DR	P-PSDB: AAY83951.
XX	

PT Interleukin 18-binding protein with activity of regulating
 PT Physiological actions of interleukin 18, useful as regulator and drug
 PT for sensitivity diseases and organ rejection and in treating diseases
 PT due to excess immune reaction
 XX
 PS Claim 6; Page 57-59; 71pp; Japanese.
 CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,
 CC and in treating autoimmune diseases. This sequence represents the coding
 CC sequence for the mature human interleukin 12 binding protein.
 XX
 SQ Sequence 492 BP; 97 A; 171 C; 136 G; 88 T; 0 other;

Query Match 100.0%; Score 492; DB 21; Length 492;
 Best Local Similarity 100.0%; Pred. No. 1.6e-116;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acactgtctgcagaccacacacagctgcactgtcctcagttagaagacaaagagcc 60
 DB 1 acactgtctgcagaccacacacagctgcactgtcctcagttagaagacaaagagcc 60
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 DB 61 tggccctccagcccccagtggttcccaagcagtaagcagtgctccagcattgtgaagc 120
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 DB 121 tggcagaagtggaagtgccactgtaagcagcgtgagcttactctgtgtggtccgagc 180
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 DB 181 cgcttcccaacttcagatcctcactgtgctgggcaatggttccctcattatgagacctc 240
 QY 241 ccaagccgactgtgggaaggagagccacgcgggaagctgtggagacacaggtatcgagctg 300
 DB 241 ccaagccgactgtgggaaggagagccacgcgggaagctgtggagacacaggtatcgagctg 300
 QY 301 tgcgaagccttgctgagcagctgacccctgcccctgcacagaccacttctcgt 360
 DB 301 tgcgaagccttgctgagcagctgacccctgcccctgcacagaccacttctcgt 360
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 DB 361 gtgtctgtgacccctgaaacaggtgtgtccagcgttcagctgtctgtggtccagcttgggct 420
 QY 421 gggtcgaaggacacttgcccccaacaaagaagccctgcctccagccacagcagttcca 480
 DB 421 gggtcgaaggacacttgcccccaacaaagaagccctgcctccagccacagcagttcca 480
 QY 481 cagcagcagaggt 492
 DB 481 cagcagcagaggt 492
 RESULT 2
 AAA11007
 ID AAA11007 standard; DNA; 744 BP.
 XX
 AC AAA11007;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human Interleukin 18 binding protein complete coding sequence.
 XX
 KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
 KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
 KW autoimmune disease; ds.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 70..654
 FT /tag= a
 FT /product= "IL-18 binding protein"
 FT sig_peptide 70..159
 FT mat_peptide 160..651
 FT /tag= b
 FT /tag= c
 WO200012555-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 18-NOV-1998; 98WO-JP05186.
 XX
 PR 01-SEP-1998; 98JP-0247588.
 PR 18-NOV-1998; 98JP-0327914.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Toriigoe K, Tanial M, Kurimoto M;
 DR WPI: 2000-237850/20.
 DR P-PSDB; AAY83985.
 XX
 PT Interleukin 18-binding protein with activity of regulating
 PT physiological actions of interleukin 18, useful as regulator and drug
 PT for sensitivity diseases and organ rejection and in treating diseases
 PT due to excess immune reaction
 XX
 PS Example 2; Page 63-64; 71pp; Japanese.
 CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,
 CC and in treating autoimmune diseases. This sequence represents the coding
 CC sequence for the full length human interleukin 12 binding protein.
 XX
 SQ Sequence 744 BP; 156 A; 249 C; 199 G; 140 T; 0 other;

Query Match 100.0%; Score 492; DB 21; Length 744;
 Best Local Similarity 100.0%; Pred. No. 1.8e-116;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acactgtctgcagaccacacacagctgcactgtcctcagttagaagacaaagagcc 60
 DB 160 acactgtctgcagaccacacacagctgcactgtcctcagttagaagacaaagagcc 219
 QY 61 tggccctccagcccccagtggttcccaagcagtaagcagtgctccagcattgtgaagc 120
 DB 220 tggccctccagcccccagtggttcccaagcagtaagcagtgctccagcattgtgaagc 279
 QY 121 tggcagaagtggaagtgccactgtaagcagcgtgagcttactctgtgtggtccgagc 180
 DB 280 tggcagaagtggaagtgccactgtaagcagcgtgagcttactctgtgtggtccgagc 339
 QY 181 cgcttcccaacttcagatcctcactgtgctgggcaatggttccctcattatgagacctc 240
 DB 340 cgcttcccaacttcagatcctcactgtgctgggcaatggttccctcattatgagacctc 399
 QY 241 ccaagccgactgtgggaaggagagccacgcgggaagctgtggagacacaggtatcgagctg 300
 DB 400 ccaagccgactgtgggaaggagagccacgcgggaagctgtggagacacaggtatcgagctg 459
 QY 301 tgcgaagccttgctgagcagctgacccctgcctgcacagaccacttctcgt 360
 DB 460 tgcgaagccttgctgagcagctgacccctgcctgcacagaccacttctcgt 519
 QY 361 gtgtctgtgacccctgaaacaggtgtgtccagcgttcagctgtctgtggtccagcttgggct 420
 DB 361 gtgtctgtgacccctgaaacaggtgtgtccagcgttcagctgtctgtggtccagcttgggct 420

Db 520 gtgctcgtgacccgtgaacaggtgtgtccagcgtcgtcgtccgtccagctctggt 579
 QY 421 gggctgaagggaacctgtgccccaccacgaagcctgtgctccctccagccacagtcaca 480
 Db 580 gggctgaagggaacctgtgccccaccacgaagcctgtgctccctccagccacagtcaca 639
 QY 481 cagcagcagaggt 492
 Db 640 cagcagcagaggt 651
 RESULT 3
 AAX24749
 ID AAX24749 standard; cDNA; 1348 BP.
 AC AAX24749;
 DT 21-JUN-1999 (first entry)
 DE Human Interleukin-18 binding protein splice variant IL-18BPA cDNA.
 XX
 KW Interleukin-18 binding protein; IL-18BP; IL-18BPA; splice variant;
 KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
 KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
 KW psoriasis; inflammatory bowel disease; multiple sclerosis;
 KW ischemic heart disease; ischemic brain injury; gene therapy; ss.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS /*tag= a
 FT 66..644
 FT /product= "IL-18BPA"
 FT sig_peptide /*tag= b
 FT 66..149
 FT mat_peptide /*tag= c
 FT 150..641
 FT /*tag= c
 PN WO9909063-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 13-AUG-1998; 98WO-IL00379.
 XX
 PR 22-JUL-1998; 98IL-0125463.
 PR 14-AUG-1997; 97IL-0121554.
 PR 27-AUG-1997; 97IL-0121639.
 PR 29-SEP-1997; 97IL-0121860.
 PR 06-NOV-1997; 97IL-0122134.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Dinarello C, Kim SH, Novick D, Rubinstein M;
 DR WPI; 1999-180975/15.
 DR P-PSDB; AAM98004.
 XX
 PT New interleukin-18 binding protein - useful for treating human
 PT diseases, including autoimmune disease and inflammation
 XX
 PS Claim 12; Page 52-53; 100pp; English.
 XX
 CC The present sequence represents a cDNA clone coding for a human
 CC interleukin-18 binding protein (IL-18BP) splice variant designated
 CC IL-18BPA (see AAM98004). This is one of 4 novel splice variants (see
 CC AAX24749-52), all coding for putative soluble proteins (see
 CC AAM98004-07), that were detected following a screening of human
 CC peripheral blood monocyte, Jurkat T-cell, peripheral blood
 CC mononuclear cell and spleen cell cDNA libraries using a probe
 CC produced using IL-18BP-specific primers. IL-18BPA is the most
 CC abundant of the 4 splice variants and is a putative member of the
 CC immunoglobulin superfamily. IL-18BP polypeptides capable of
 CC binding IL-18 and/or modulating and/or blocking IL-18 activity are

CC provided. Methods for their isolation and recombinant production,
 CC DNA vectors expressing them, vectors useful for their expression in
 CC humans and other mammals, and antibodies against them are also
 CC provided. IL-18BP polypeptides, and DNA encoding them, can be used
 CC to treat conditions requiring the protein (claimed). Conditions
 CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,
 CC graft rejections, inflammatory bowel disease, sepsis, multiple
 CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic
 CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
 CC also useful for purifying IL-18 (claimed).
 XX
 SQ Sequence 1348 BP; 304 A; 449 C; 292 G; 303 T; 0 other;
 Query Match 100.0%; Score 492; DB 20; Length 1348;
 Best Local Similarity 100.0%; Pred. No. 2.1e-116;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 acacctgtctcgagaccacacacagctgcacgtgctcctcaagttagaagacaaagacc 60
 Db 150 acacgtgtctcgagaccacacacagctgcacgtgctcctcaagttagaagacaaagacc 209
 QY 61 tgcctctccagcccccagctgttcccaagcagtaagcagtgctccagcattggaagtacc 120
 Db 210 tgcctctccagcccccagctgttcccaagcagtaagcagtgctccagcattggaagtacc 269
 QY 121 tggcagaggttggaagtgcacactgaatggaagctgtatctgtgtgtgacctgagc 180
 Db 270 tggcagaggttggaagtgcacactgaatggaagctgtatctgtgtgtgacctgagc 329
 QY 181 cgcttcccaacttcagacatccttactagctgtgcaatgttccctcatctgacacctc 240
 Db 330 cgcttcccaacttcagacatccttactagctgtgcaatgttccctcatctgacacctc 389
 QY 241 ccagcccgactgtggaaggagacacagccgggaagctgtgagacagagtaacgacgtg 300
 Db 390 ccagcccgactgtggaaggagacacagccgggaagctgtgagacagagtaacgacgtg 449
 QY 301 tgcgaagccttggtgtcgtgagcagctgacccctgacctgacagacaaacttctctgt 360
 Db 450 tgcgaagccttggtgtcgtgagcagctgacccctgacctgacagacaaacttctctgt 509
 QY 361 gtgctcgtgacccgtgaacaggtgtgtccagcgtcagctgtctgtgcccagctctggt 420
 Db 510 gtgctcgtgacccgtgaacaggtgtgtccagcgtcagctgtctgtgcccagctctggt 569
 QY 421 gggctgaagggaacctgtgccccaccacgaagcctgtgctccctccagccacagtcaca 480
 Db 570 gggctgaagggaacctgtgccccaccacgaagcctgtgctccctccagccacagtcaca 629
 QY 481 cagcagcagaggt 492
 Db 630 cagcagcagaggt 641
 RESULT 4
 AAX27384
 ID AAX27384 standard; cDNA; 1356 BP.
 AC AAX27384;
 DT 16-AUG-2000 (first entry)
 DE Human IGFAM-4 immunoglobulin coding sequence.
 XX
 KW Human; immunoglobulin; IGFAM-4; IGFAM; immune disorder; cancer;
 KW infection; inflammation; haematopoiesis; AIDS; allergy; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 92..676
 FT /*tag= a

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FT      sig_peptide      /product= "IGFAM-4"
FT      mat_peptide      /*tag= b
FT      242..673         /*tag= c
FT      WO200029583-A2.
XX      25-MAY-2000.
XX      19-NOV-1999;      99WO-US27566.
XX      19-NOV-1998;      99US-0113635.
XX      22-DEC-1998;      98US-0113635.
XX      07-APR-1999;      99US-0128194.
XX      (INCY-) INCYTE PHARM INC.
XX      Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
XX      Lu DM, Lal P, Hillman JL, Yang J;
XX      WPI: 2000-387796/33.
XX      P-PSDB: AAY96292.
XX      Immunoglobulin superfamily proteins, the agonist and antagonist of the
XX      protein is useful for preventing and treating disorders associated with
XX      altered levels of the protein such as cancer, immune system disorders
XX      Claim 9; Page 96; 105pp; English.
XX      The present sequence is the human immunoglobulin superfamily protein
XX      IGFAM-4 gene, which was isolated from a cDNA library of prostate tumour
XX      tissue. It is expressed in nervous, haematopoietic and immune and
XX      cardiovascular tissue, where cancer and inflammation are common. The
XX      gene, protein, its antibodies, agonists and antagonists are suitable for
XX      diagnosing and treating many diseases, including cancer, immune system
XX      disorders (such as inflammation, AIDS, allergies, anaemia,
XX      arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
XX      disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
XX      multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
XX      systemic lupus erythematosus and ulcerative colitis), complications of
XX      cancer, haemodialysis and extracorporeal circulation, trauma and
XX      haematopoietic cancer (such as leukaemia) and infections caused by
XX      bacteria, viruses, fungi or parasites.
XX      Sequence 1356 BP; 282 A; 458 C; 305 G; 311 T; 0 other;
SQ

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Query Match      100.0%; Score 492; DB 21; Length 1356;
Best Local Similarity 100.0%; Pred. NO. 2.1e-116;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 acacgtgtctgcagaccacacagctgtccactgctcactagtagaagacaaagacccc 60
DB      182 acactgtctgcagaccacacacagctgtccactgctcactagtagaagacaaagacccc 241
QY      61 tgcctctccagcccccagctgttccagcagctaagcaggttccaagattggaagtgc 120
DB      242 tgcctctccagcccccagctgttccagcagctaagcaggttccaagattggaagtgc 301
QY      121 tgcacagagtgtgaagctccactgaatgaagcgtgaagctatccctgtgtgctgcagc 180
DB      302 tgcacagagtgtgaagctccactgaatgaagcgtgaagctatccctgtgtgctgcagc 361
QY      181 cgtctcccaacttcagatcctctactgtgtgtgcaatgttctctcatgagacatc 240
DB      362 cgtctcccaacttcagatcctctactgtgtgtgcaatgttctctcatgagacatc 421
QY      241 ccaggtccgactgtgtgagggagacacagccggaacgtgtggaagcacaggtacgactgt 300
DB      422 ccaggtccgactgtgtgagggagacacagccggaacgtgtggaagcacaggtacgactgt 481

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QY      301 tgcagagccttgctgtcgtgagcagctgacccctgcctgcagacagcaacttctctgt 360
DB      482 tgcagagccttgctgtcgtgagcagctgacccctgcctgcagacagcaacttctctgt 541
QY      361 gtgtctgtgacccttbaacaggtgtcagcgttaeagtgtctgtgcccagcttgggt 420
DB      542 gtgtctgtgacccttbaacaggtgtcagcgttaeagtgtctgtgcccagcttgggt 601
QY      421 gggctgagggcaaccttgcctcccccacaaagagccctgcctccagccagcagtcaca 480
DB      602 gggctgagggcaaccttgcctcccccacaaagagccctgcctccagccagcagtcaca 661
QY      481 cagcagcagaggt 492
DB      662 cagcagcagaggt 673

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RESULT 5

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ID      AAX24751
ID      AAX24751 standard; cDNA; 7063 BP.
AC      AAX24751;

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DE      21-JUN-1999 (first entry)

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XX      Human interleukin-18 binding protein splice variant IL-18Bpc cDNA.
XX      Interleukin-18 binding protein; IL-18BP; IL-18Bpc; splice variant;
XX      human; autoimmune disease; inflammation; diabetes; pancreatitis;
XX      rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
XX      psoriasis; inflammatory bowel disease; multiple sclerosis;
XX      ischemic heart disease; ischemic brain injury; gene therapy; ss.
XX      Homo sapiens.
XX      OS

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FH      Key      Location/Qualifiers
FT      CDS      949..1542
FT      /*tag= a
FT      /product= "IL-18Bpc"
FT      sig_peptide 949..1032
FT      /*tag= b
FT      mat_peptide 1033..1539
FT      /*tag= c

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XX      W09909063-A1.
XX      PN
XX      25-FEB-1999.
XX      PD

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XX      PF      13-AUG-1998;      98WO-IL00379.
XX      PR      22-JUL-1998;      98IL-0125463.
XX      PR      14-AUG-1997;      97IL-0121554.
XX      PR      27-AUG-1997;      97IL-0121639.
XX      PR      29-SEP-1997;      97IL-0121860.
XX      PR      06-NOV-1997;      97IL-0122134.
XX      PA

```

```

XX      (YEDA ) YEDA RES & DEV CO LTD.
XX      PI
XX      Dinarello C, Kim SH, Novick D, Rubinstein M;
XX      DR

```

```

XX      WPI: 1999-180975/15.
XX      P-PSDB: AAW98006.
XX      DR

```

```

XX      New interleukin-18 binding protein - useful for treating human
XX      diseases, including autoimmune disease and inflammation
XX      Claim 12; Page 55-58; 100pp; English.
XX      PS

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```

XX      The present sequence represents a cDNA clone coding for a human
XX      interleukin-18 binding protein (IL-18BP) splice variant designated
XX      IL-18Bpc (see AAW98006). This is one of 4 novel splice variants (see
XX      AAX24749-52), all coding for putative soluble proteins (see
XX      AAW98004-07), that were detected following a screening of human

```

CC peripheral blood monocyte, Jurkat T-cell, peripheral blood
 CC mononuclear cell and spleen cell cDNA libraries using a probe
 CC produced using IL-18BP-specific primers. IL-18BP is a low
 CC abundance splice variant. IL-18BP polypeptides capable of
 CC binding IL-18 and/or modulating and/or blocking IL-18 activity are
 CC provided. Methods for their isolation and recombinant production,
 CC DNA vectors expressing them, vectors useful for their expression in
 CC humans and other mammals, and antibodies against them are also
 CC provided. IL-18BP polypeptides, and DNA encoding them, can be used
 CC to treat conditions requiring the protein (claimed). Conditions
 CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,
 CC graft rejections, inflammatory bowel disease, sepsis, multiple
 CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic
 CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
 CC also useful for purifying IL-18 (claimed).

XX
 SQ Sequence 7063 BP; 1538 A; 2025 C; 1981 G; 1519 T; 0 other;

Query Match 85.0%; Score 418.2; DB 20; Length 7063;
 Best Local Similarity 99.3%; Pred. No. 2.5e-97;
 Matches 420; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 acacgtgtctcgagaccacacacagctgcacgtcctcagttagaagacacaaagagcccc 60
 Db 1033 acacgtgtctcgagaccacacacagctgcacgtcctcagttagaagacacaaagagcccc 1092
 QY 61 tggccctccagcccccaatgtttccagacagctaaagcaatgttccacatttggaagtgacc 120
 Db 1093 tggccctccagcccccaatgtttccagacagctaaagcaatgttccacatttggaagtgacc 1152
 QY 121 tggcagaggtggaagtgcacactgaatggaacgtgagcttaccctgtgtgacctcagc 180
 Db 1153 tggcagaggtggaagtgcacactgaatggaacgtgagcttaccctgtgtgacctcagc 1212
 QY 181 cgcttcccaacttcagcaltcctactctgctggtggaatggttccctcatltgagcacctc 240
 Db 1213 cgcttcccaacttcagcaltcctactctgctggtggaatggttccctcatltgagcacctc 1272
 QY 241 ccagggccgactgtggagagggagacacacacgggaacgtgggagagacagtgagcagctg 300
 Db 1273 ccagggccgactgtggagagggagacacacacgggaacgtgggagagacagtgagcagctg 1332
 QY 301 tgcgaagccttggtgtgtagcagctgacccctgaccttcacagacacaaactctctctgt 360
 Db 1333 tgcgaagccttggtgtgtagcagctgacccctgaccttcacagacacaaactctctctgt 1392
 QY 361 gtgtcgttgagacctgaacaggttgcacagctacagctgcctctgagccagctctggact 420
 Db 1393 gtgtcgttgagacctgaacaggttgcacagctgcctctgagccagctctggact 1452
 QY 421 ggg 423
 Db 1453 agg 1455

RESULT 6

AAAI1004
 ID AAAI1004 standard; DNA; 411 BP.

XX AAAI1004;
 DT 28-JUL-2000 (first entry)
 XX

DE Human IL-18 binding protein 5' RACE fragment #1.

XX
 KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
 KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
 KW autoimmune disease; rapid amplification of cDNA ends; RACE; ss.

OS Homo sapiens.

XX
 FH Key Location/Qualifiers

FT CDS 1..411
 FT /tag= a
 FT /partial
 FT /note="fragment of N-terminus of IL-18 binding protein"

PN WO200012555-A1.

XX 09-MAR-2000.

PF 18-NOV-1998; 98WO-JP05186.

XX 01-SEP-1998; 98JP-0247588.

PR 18-NOV-1998; 98JP-0327914.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Toriigoe K, Tanai M, Kurimoto M;

DR WPI; 2000-237850/20.

DR P-PSDB; AAY83982.

PT Interleukin 18-binding protein with activity of regulating

PT physiological actions of interleukin 18, useful as regulator and drug

PT for sensitivity diseases and organ rejection and in treating diseases

PT due to excess immune reaction

PS Example 2; Page 60-61; 71pp; Japanese.

XX The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,
 CC and in treating autoimmune diseases. This sequence represents the initial
 CC fragment isolated by a 5' RACE (Rapid Amplification of cDNA Ends)
 CC reaction for the 5' end of the interleukin 12 binding protein coding
 CC sequence.

XX
 SQ Sequence 411 BP; 81 A; 138 C; 114 G; 78 T; 0 other;

Query Match 83.5%; Score 411; DB 21; Length 411;
 Best Local Similarity 100.0%; Pred. No. 8.1e-96;
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acacgtgtctcgagaccacacacagctgcacgtcctcagttagaagacacaaagagcccc 60
 Db 1 acacgtgtctcgagaccacacacagctgcacgtcctcagttagaagacacaaagagcccc 60
 QY 61 tggccctccagcccccaatgtttccagacagctaaagcaatgttccacatttggaagtgacc 120
 Db 61 tggccctccagcccccaatgtttccagacagctaaagcaatgttccacatttggaagtgacc 120
 QY 121 tggcagaggtggaagtgcacactgaatggaacgtgagcttaccctgtgtgacctcagc 180
 Db 121 tggcagaggtggaagtgcacactgaatggaacgtgagcttaccctgtgtgacctcagc 180
 QY 181 cgcttcccaacttcagcaltcctactctgctggtggaatggttccctcatltgagcacctc 240
 Db 181 cgcttcccaacttcagcaltcctactctgctggtggaatggttccctcatltgagcacctc 240
 QY 241 ccagggccgactgtggagagggagacacacacgggaacgtgggagagacagtgagcagctg 300
 Db 241 ccagggccgactgtggagagggagacacacacgggaacgtgggagagacagtgagcagctg 300
 QY 301 tgcgaagccttggtgtgtagcagctgacccctgaccttcacagacacaaactctctctgt 360
 Db 301 tgcgaagccttggtgtgtagcagctgacccctgaccttcacagacacaaactctctctgt 360
 QY 361 gtgtcgttgagacctgaacaggttgcacagctacagctgcctctgagccagctctggact 411
 Db 361 gtgtcgttgagacctgaacaggttgcacagctacagctgcctctgagccagctctggact 411

```

RESULT 7
AA24752
ID AAX24752 standard; cDNA; 1360 BP.
XX
AC AAX24752;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human Interleukin-18 binding protein splice variant IL-18BPd cDNA.
XX
KW Interleukin-18 binding protein; IL-18BP; IL-18BPd; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
KW ischemic heart disease; ischemic brain injury; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 169..654
FT /tag= a
FT /product= "IL-18BPd"
FT sig_peptide 169..252
FT /tag= b
FT mat_peptide 253..651
FT /tag= c
XX
PN MO909063-A1.
XX
PD 25-FEB-1999.
XX
PE 13-AUG-1998; 98WO-IL00379.
XX
PR 22-JUL-1998; 98IL-0125463.
PR 14-AUG-1997; 97IL-0121554.
PR 27-AUG-1997; 97IL-0121639.
PR 29-SEP-1997; 97IL-0121860.
PR 06-NOV-1997; 97IL-0122134.
XX
PA (YEDA ) YEDA RES & DEV CO LTD.
XX
PI Dlnarello C, Kim SH, Novick D, Rubinstein M,
XX
DR WPI: 1999-180975/15.
XX
P-PSDB; AAM98007.
XX
PT New interleukin-18 binding protein - useful for treating human
PT diseases, including autoimmune disease and inflammation
XX
PS Claim 12; Page 59; 100pp; English.
XX
XX
XX The present sequence represents a cDNA clone coding for a human
XX interleukin-18 binding protein (IL-18BP) splice variant designated
XX IL-18BPd (see AAM98007). This is one of 4 novel splice variants (see
XX AAX24749-52), all coding for putative soluble proteins (see
XX AAM98004-07), that were detected following a screening of human
XX peripheral blood monocyte, Jurkat T-cell, peripheral blood
XX mononuclear cell and spleen cell cDNA libraries using a probe
XX produced using IL-18BP-specific primers. IL-18BPd is a low
XX abundance splice variant. IL-18BP polypeptides capable of
XX binding IL-18 and/or modulating and/or blocking IL-18 activity are
XX provided. Methods for their isolation and recombinant production,
XX DNA vectors expressing them, vectors useful for their expression in
XX humans and other mammals, and antibodies against them are also
XX provided. IL-18BP polypeptides, and DNA encoding them, can be used
XX to treat conditions requiring the protein (claimed). Conditions
XX include autoimmune diseases, type I diabetes, rheumatoid arthritis,
XX graft rejections, inflammatory bowel disease, sepsis, multiple
XX sclerosis, ischemic heart diseases, ischemic brain injury, chronic
XX hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
XX also useful for purifying IL-18 (claimed).
XX
XX Sequence 1360 BP; 289 A; 454 C; 303 G; 314 T; 0 other;
XX

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```

Query Match 59.1%; Score 290.6; DB 20; Length 1360;
Best Local Similarity 97.0%; Pred. No. 7.1e-65;
Matches 296; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 aacactgtctgcagagccacccacagctgcacatgtcctagttagaagcacaaagacccc 60
DB 253 aacactgtctgcagagccacccacagctgcacatgtcctagttagaagcacaaagacccc 312
QY 61 tgcctccccaagcccccagctgttcccaagagtaagcaagtgcagcattggaagtacc 120
DB 313 tgcctccccaagcccccagctgttcccaagagtaagcaagtgcagcattggaagtacc 372
QY 121 tggccagaggtggaagtgcacactgaatggaacgtcgaacttaccgtgtggtgcgcagc 180
DB 373 tggccagaggtggaagtgcacactgaatggaacgtcgaacttaccgtgtggtgcgcagc 432
QY 181 cgttccccaacttcagatcctctactgctggtgcaatggttcttcaattgagcctc 240
DB 433 cgttccccaacttcagatcctctactgctggtgcaatggttcttcaattgagcctc 492
QY 241 ccaggcgactgtggagggagagccacagccggagcgtggagagcacagtaacgagctg 300
DB 493 ccaggcgactgtggagggagagccacagccggagcgtggagagcacagtaacgagctg 552
QY 301 tgcaa 305
DB 553 ggcac 557

RESULT 8
AA11003
ID AA11003 standard; DNA; 495 BP.
XX
AC AA11003;
XX
DT 28-JUL-2000 (first entry)
XX
DE Mouse mature Interleukin 18 binding protein coding sequence.
XX
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease; ss.
XX
OS Mus musculus.
XX
PN W0200012555-A1.
XX
PD 09-MAR-2000.
XX
PE 18-NOV-1998; 98WO-JP05186.
XX
PR 01-SEP-1998; 98JP-0247588.
PR 18-NOV-1998; 98JP-0327914.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Torioge K, Tanai M, Kurimoto M;
XX
DR WPI: 2000-237850/20.
XX
XX
XX Interleukin 18-binding protein with activity of regulating
XX physiological actions of interleukin 18, useful as regulator and drug
XX for sensitivity diseases and organ rejection and in treating diseases
XX due to excess immune reaction -
XX
XX Claim 6; Page 57-59; 71pp; Japanese.
XX
XX The invention relates to novel interleukin 18 (IL-18)-binding proteins
XX from humans or mice which act as regulators and drugs for sensitivity
XX diseases and organ rejection and in treating diseases due to excess
XX immune reaction, e.g. in slowing down rejection after organ transplant,
XX

```


CC disease), tumours, bacterial, fungal or viral infections, depression and
CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given
CC in the exemplification of the present invention.

SQ Sequence 495 BP; 117 A; 151 C; 119 G; 108 T; 0 other;

Query Match	40.2%	Score 197.8	DB 21	Length 495
Best Local Similarity	78.2%	Pred. No. 3e-41		
Matches 251	Conservative 0	Mismatches 67	Indels 3	Gaps 1

OY	22	acagcttccgaactgctctaagttaagagagacaaaggaccccttgcctctccagccccaagt	81
Db	175	acaactgcgaatgctcttaactggaagctcaaaagaacccaagctctcttcgtgctccagca	234
OY	82	ttccacagcagctaaagcagctgtccagcacttggaagtgcacctgcgcagaagtgtgaatgtcca	141
Db	235	gtcccaag--taagcagtaaccagcagctctgagtgtgatctgcagaaaaagaagtcca	293
OY	142	ctgaatgtgaacgcgtgaactatctctgtgtgacctgcagcagcttccccaacttcagatc	201
Db	292	ctgaatgtgaactctgcgaactgttccctgtgaactgcgcagcagcgtctccctacttcagatc	351
OY	202	ctctactgtgctbvggcaaatgtgtcccttcattgaagaccttcccaagcgcagctgttggaagg	261
Db	352	ctctactgtgctbvggcaaatgtgtcccttcattgaagaccttcccaagcgcagctgttggaagg	411
OY	262	agcacccagccggagaacgttgtagagacaggtacgaagtgtgcaagagcttgtgtgtgtgag	321
Db	412	cacccaagtctggagagcaacagacaagaacacgacactgtgtctgcacagagcttctgtgtgaa	471
OY	322	caagctgaacccttgcctctgcaac	342
Db	472	caactgtgagcccaaccaatc	492

RESULT	12
AAX24753	
ID	AAX24753 standard; cDNA; 7812 BP.

AC AAX24753;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human interleukin-18 binding protein gene.

KM Interleukin-18 binding protein; IL-18BP; IL-18BPb; splice variant;
KM human; autoimmune disease; inflammation; diabetes; pancreatitis;
KM rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KM psoriasis; inflammatory bowel disease; multiple sclerosis;
KM ischemic heart disease; ischemic brain injury; gene therapy; ss.

OS Homo sapiens.

PN W09909063-A1.

PD 25-FEB-1999.

PF 13-AUG-1998; 98WO-IL00379.

PR 22-JUL-1998; 98TL-0125463.

PR	27-AUG-1997;	97IL-0121639.
PR	14-AUG-1997;	97IL-0121334.

PR	29-SEP-1997	97IL-0121860
PR	06-NOV-1997	97IL-0122134

XX
PA (YEDA) YEDA RES & DEV CO LT

XX	Dinarelli C	Kim SH	Novic
PI			

XX WPT: 1999-180975/15

XX
XX
Now factor out 10. If 27 is

PT	diseases, including autoimmune disease and inflammation
XX	
PS	Disclosure; Page 60-63; 100pp; English.

The present sequence comprises human interleukin-18 binding protein (IL-18BP) genomic DNA. It was produced from 5 genomic clones isolated from a human genomic library by screening with full-length human IL-18BP cDNA. No exon coding for a transmembrane receptor was identified within the 7.8 kb sequence. 4 Splice variant clones (see AAX24749-52) were identified that code for putative soluble secreted proteins, designated IL-18BP-a (see AAM98004-007). The IL-18BP locus contains an additional gene, coding for the nuclear mitotic apparatus protein 1 (NMAP1), positioned on the minus strand CC This localised the IL-18BP gene to human chromosome 11q13(36). CC IL-18BP polypeptides capable of binding IL-18 and/or modulating CC and/or blocking IL-18 activity are provided by the invention. CC Methods for their isolation and recombinant production, DNA vectors CC expressing them, vectors useful for their expression in humans and CC other mammals, and antibodies against them are also provided. CC IL-18BP polypeptides, and DNA encoding them, can be used to treat CC conditions requiring the protein (claimed). Such conditions CC include autoimmune diseases, type I diabetes, rheumatoid arthritis, CC graft rejections, inflammatory bowel disease, sepsis, multiple CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is CC also useful for purifying IL-18(claimed).

SQ Sequence 7812 BP; 1689 A; 2278 C; 2167 G; 1678 T; 0 other;

Query Match	38.1%	Score 187.6;	DB 20;	Length 7812;
Best Local Similarity	74.58;	Pred. No. 2.5e-38;		
Matches 289; Conservative	0;	Mismatches 19;	Indels 80;	Gaps 11;

QY	116	tgatctgcccagaggtgtagaagttccacttgaatgaaagcgttgaagcttatccctgttggcct	175
Db	1863	tgaaagagctatactgcgtcgtcgtgttcccttgaagtagaaagcttgaagcttatccctgttggcct	1922
QY	176	gcaacgcgcctctccccaacttcaagcatccctctactgtgcttgggcaatggttctctcatttgagc	235
Db	1923	gcagcgcgtctccccaacttcaagcatccctctactgtgcttgggcaatggttctctcatttgagc	1982
QY	236	acctccccaaggcagactgtgtgtagagggagga-----	265
Db	1983	acctccccaaggcagactgtgtgtagagggaggaacccaagttgaaggtctcgacagccaagtgtgct	2042
QY	266	-----ccaagccggga	275
Db	2043	gggaaggaagccttcctgcgcctctccatgaaaccttctctccctccgcctccagccggga	2102
QY	276	acgtgtaggaagacaaggttagcagagctgtgcaagaagcctgtgtgcctggtagcagacttgaacccctgc	335
Db	2103	acgtgtaggaagacaaggttagcagagctgtgcaagaagcctgtgtgtcctggtagcagacttgaacccctgc	2162
QY	336	ccttgcacagcacacaactctccctctgtgtgtcctctgtgaaccccttgaacagagttgttccagctga	395
Db	2163	ccttgcacagcacacaactctccctctgtgtgtcctctgtgaaccccttgaacagagttgttccagctga	2222

RESULT	13
AAS70037/c	
ID	AAS70037 standard; cDNA; 6741 BP

AC AAS70037;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #5841.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB: ABG05850.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 5841; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 6741 BP; 1764 A; 1725 C; 2134 G; 1117 T; 1 other;

Query Match 30.9%; Score 152; DB 23; Length 6741;
Best Local Similarity 94.0%; Pred. No. 3.1e-29;
Matches 158; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 263 gcaccagccgggaacgtgaggacaggtacgacgtgtgaagccctgtgtcgtgagc 322
DB 1514 GCTCCAGCCGGGAGAGCTGGAGACAGGTACGACGCTGTGCAAGCCTTGGTGGAGC 1455
QY 323 agctgacccctgccttgacagcacaactctctctgtgtgtcgtgtgacccctgacagg 382
DB 1454 AGCTGACCCCTGCCTGACAGACCAACTTCTCTGTGTGTCTGTGACCTGTGAACAG 1395
QY 383 ttgtccagcgtcaacgtcgtctcgtgcccagcgtcgtggtcgtgagcgtgagg 430
DB 1394 TTGTCACAGCTACGCTCTCTCTGCGCCAGCTTGGCTTGGCTCGAGGG 1347

RESULT 14
AAS70676/c
ID AAS70676 standard; CDNA: 7103 BP.

XX
AC AAS70676;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #6480.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB: ABG06489.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 6480; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 7103 BP; 1879 A; 1805 C; 2233 G; 1185 T; 1 other;

Query Match 30.9%; Score 152; DB 23; Length 7103;
Best Local Similarity 94.0%; Pred. No. 3.2e-29;
Matches 158; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 263 gcaccagccgggaacgtgaggacaggtacgacgtgtgaagccctgtgtcgtgagc 322
DB 1876 GCTCCAGCCGGGAGAGCTGGAGACAGGTACGACGCTGTGCAAGCCTTGGTGGAGC 1817
QY 323 agctgacccctgccttgacagcacaactctctctgtgtgtcgtgtgacccctgacagg 382
DB 1816 AGCTGACCCCTGCCTGACAGACCAACTTCTCTGTGTGTCTGTGACCTGTGAACAG 1757
QY 383 ttgtccagcgtcaacgtcgtctcgtgcccagcgtcgtggtcgtgagcgtgagg 430

Db 1058 TGTGCGCCGAGAGCGCCGACCGCGATCCGCGACACTGTGCTGTCGCCGTGCG 1117
OY 371 accctgaacaggtgtccacgctcagctcgtcgtccagctcgtggtcgtgaagg 430
Db 1118 GCCTGGAAGACGTGTGACCTCAAGCGGACCTGCGCGTGGCTGGCGGCGCTGTGAG 1177
OY 431 caacttgcccccaacc 448
Db 1178 GACGGGGGCCCGCGTTCC 1195

RESULT 2

US-09-479-409-29
Sequence 29, Application US/09479409
Patent No. 6225106
GENERAL INFORMATION:
APPLICANT: Gerltse, Gijshert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,409
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gjalster, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 17612 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-479-409-29

Query Match 7.9%; Score 38.8; DB 4; Length 17612;
Best Local Similarity 55.1%; Pred. No. 0.37; Mismatches 62; Indels 0; Gaps 0;
Matches 76; Conservative 0;

OY 311 tgggtcgtgagcagctgacccctgcctgcacagcaccacacttcctcgtgtgctcgtg 370
Db 1058 TGTGCGCCGAGAGCGCCGACCGCGATCCGCGACACTGTGCTGTCGCCGTGCG 1117
OY 371 accctgaacaggtgtccacgctcagctcgtcgtccagctcgtggtcgtgaagg 430
Db 1118 GCCTGGAAGACGTGTGACCTCAAGCGGACCTGCGCGTGGCTGGCGGCGCTGTGAG 1177
OY 431 caacttgcccccaacc 448
Db 1178 GACGGGGGCCCGCGTTCC 1195

RESULT 3

US-09-479-453-29
Sequence 29, Application US/09479453
Patent No. 6313283
GENERAL INFORMATION:
APPLICANT: Gerltse, Gijshert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,453
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gjalster, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 17612 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-479-453-29

Query Match 7.9%; Score 38.8; DB 4; Length 17612;
Best Local Similarity 55.1%; Pred. No. 0.37; Mismatches 62; Indels 0; Gaps 0;
Matches 76; Conservative 0;

OY 311 tgggtcgtgagcagctgacccctgcctgcacagcaccacacttcctcgtgtgctcgtg 370
Db 1058 TGTGCGCCGAGAGCGCCGACCGCGATCCGCGACACTGTGCTGTCGCCGTGCG 1117
OY 371 accctgaacaggtgtccacgctcagctcgtcgtccagctcgtggtcgtgaagg 430
Db 1118 GCCTGGAAGACGTGTGACCTCAAGCGGACCTGCGCGTGGCTGGCGGCGCTGTGAG 1177
OY 431 caacttgcccccaacc 448
Db 1178 GACGGGGGCCCGCGTTCC 1195

RESULT 4
US-08-804-227C-7
Sequence 7, Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: Dehoff, Bradley S.
APPLICANT: Kustoss, Stuart A.
APPLICANT: Kosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501

```

; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII(DOS) Text only
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,227C
; FILING DATE: February 21, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plant, Thomas, G.
; REGISTRATION NUMBER: 35,784
; REFERENCE/DOCKET NUMBER: X-8231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-2459
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 350..14002
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14046..20036
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20110..31284
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31329..36071
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 36155..41830
; US-08-804-227C-7

Query Match          7.8%; Score 38.2; DB 2; Length 44377;
Best Local Similarity 53.7%; Pred. No. 0.69;
Matches 79; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 330 ccctgcccgcacagacacaaactctctgtgtgtgctggaacccctgaacaggtgtcca 389
    || || || || || || || || || || || || || || || || || || || || ||
DB 31083 CACCCCCGAGCAGCTGCGGAGCTCGCCCCCGCCGACGACCGGGCGGAGTCCCTT 31142

QY 390 ggcgtacgctgcgtcgtgcccagctctggcctgagctgagggcaacctggccccaccca 449
    || || || || || || || || || || || || || || || || || || || || ||
DB 31143 GCGCCCTGGAGCGCTGCGGAGCTGCGGCGCTGCGACGACGAGCGCGCCGCGCGCGA 31202

QY 450 agaagccctgcctcagccacagcag 476
    || || || || || || || || || || || || || || || || || || || || ||
DB 31203 CGACGACATCACCAGAGCTGTGAGCAG 31229

RESULT 5
US-08-804-198-1
; Sequence 1, Application US/08804198
; Patent No. 5945320
; GENERAL INFORMATION:
; APPLICANT: Burgett, Stanley G.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rao, Nagaraja R.
; APPLICANT: Richardson, Mark A.
; APPLICANT: Rostek, Paul R., Jr.
; TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE

```

```

; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PAUL R. CANTRELL, 1138
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,198
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CANTRELL, PAUL R.
; REGISTRATION NUMBER: 36,470
; REFERENCE/DOCKET NUMBER: P9113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3885
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 350..14002
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14046..20036
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20110..31284
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31329..36071
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 36155..41830
; US-08-804-198-1

Query Match          7.8%; Score 38.2; DB 2; Length 44377;
Best Local Similarity 53.7%; Pred. No. 0.69;
Matches 79; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 330 ccctgcccgcacagacacaaactctctgtgtgtgctggaacccctgaacaggtgtcca 389
    || || || || || || || || || || || || || || || || || || || || ||
DB 31083 CACCCCCGAGCAGCTGCGGAGCTCGCCCCCGCCGACGACCGGGCGGAGTCCCTT 31142

QY 390 ggcgtacgctgcgtcgtgcccagctctggcctgagctgagggcaacctggccccaccca 449
    || || || || || || || || || || || || || || || || || || || || ||
DB 31143 GCGCCCTGGAGCGCTGCGGAGCTGCGGCGCTGCGACGACGAGCGCGCCGCGCGCGA 31202

QY 450 agaagccctgcctcagccacagcag 476
    || || || || || || || || || || || || || || || || || || || || ||
DB 31203 CGACGACATCACCAGAGCTGTGAGCAG 31229

RESULT 6
US-09-057-860A-1
; Sequence 1, Application US/09057860A
; Patent No. 6277820
; GENERAL INFORMATION:
; APPLICANT: Arnon Rosenthal
; APPLICANT: Mary Hynes
; APPLICANT: Weilan Ye

```

```

; TITLE OF INVENTION: Method Of Dopaminergic And Seratonergic
; TITLE OF INVENTION: Neuron Formation From Neuroprogenitor Cells
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatlin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,860A
; FILING DATE: 09-Apr-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1364
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Circular
;
US-09-057-860A-1
```

```

Query Match          7.4%; Score 36.6; DB 4; Length 609;
Best Local Similarity 49.7%; Pred. No. 0.53;
Matches 93; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 282 gagcaagtagcagctgtgcaagcctgtgtgtagcagctgacccctgcctga 341
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 18 GACCACAGGAGGAGCTGCTGACGAGGCTCTGCTGCTGCTGCTGCTGCTGCTG 77

QY 342 cagaccacactctccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 401
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 78 AGGACCGCGCCGACCAACGACGACGACGACGACGACGACGACGACGACGACG 137

QY 402 cctggccagctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 461
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 138 GGTGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 197

QY 462 ctccagc 468
    |||||
Db 198 CAGCGGC 204

RESULT 7
US-09-105-537-7
; Sequence 7, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1248
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```

; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
;
US-09-105-537-7
```

```

Query Match          7.4%; Score 36.2; DB 4; Length 1248;
Best Local Similarity 47.5%; Pred. No. 0.83;
Matches 143; Conservative 0; Mismatches 153; Indels 5; Gaps 1;

QY 184 ttccccaactcagcatcctcctactgctggtggcaatgttcttcattgagacctcca 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 775 ttcccgaggtcatcagccggaacccggaacccggaacccggaacccggaacccgga 834

QY 244 ggcgcactgtggtggtggtggtggtggtggtggtggtggtggtggtggtg 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 835 gaccctcccggtctcgtctcgtctcgtctcgtctcgtctcgtctcgtctcgtctc 894

QY 304 aagccttggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 895 gtgacgtcagatcagcagaggtccacacgtgtgtgtgtgtgtgtgtgtgtgtgtgt 954

QY 364 ctctgtgac-----cctgaacaggtgtgtccagcgtcgtctgtgtgtgtgtgtgtgt 418
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 955 ctgaaggtcgaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1014

QY 419 ctgggtgtggtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 478
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1015 cgtaccggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1074

QY 479 c 479
Db 1075 c 1075
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```

RESULT 8
US-09-105-537-3/c
; Sequence 3, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 13613
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
;
US-09-105-537-3
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```

Query Match          7.4%; Score 36.2; DB 4; Length 13613;
Best Local Similarity 47.5%; Pred. No. 1.6;
Matches 143; Conservative 0; Mismatches 153; Indels 5; Gaps 1;

QY 184 ttccccaactcagcatcctcctactgctggtggcaatgttcttcattgagacctcca 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12109 TTTCCTCCGAGGTGATCGACGCGGACCGGACCGGACCGGACCGGACCGGACCGG 12050

QY 244 ggcgcactgtggtggtggtggtggtggtggtggtggtggtggtggtggtg 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12049 GACCTCCCGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11990

QY 304 aagccttggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11989 GTATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 11930

QY 364 ctctgtgac-----cctgaacaggtgtgtcagcgtcagcgtcgtcgtcgtcgtcgtcgt 418
```

Db 11929 CTGAAGCCGAGGCGGACACCGGCGCTACTTCTCGCGGGGCTGCCACGAGCTGGAG 11870
 QY 419 ctgggctgaggggaacctgtgcccccccaagaagcctgtccctcagccacagcagtc 478
 Db 11869 CCTTACCGGGGAGCGACGCCCGCTGCCACACGAGCGCTCGCGCGCGGTG 11810
 QY 479 c 479
 Db 11809 c 11809

RESULT 9
 US-09-103-840A-1
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4411529
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; OTHER INFORMATION: H37Rv
 US-09-103-840A-1

Query Match 7.3%; Score 36; DB 4; Length 4411529;
 Best Local Similarity 55.6%; Pred. No. 9;
 Matches 69; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
 QY 307 gccctgtgtctgagcagctgaccctgccctgcacagcacaactctctctgtgtctc 366
 Db 4156424 gacattgtgcgcagcagatgtgcgcgcgcagcagcagctgcgaacactccgcgcatatc 4156483
 QY 367 gtggaccctgaagaggtgtccagcgttcacgttctcctgcccagcttctgggtggcgtg 426
 Db 4156484 ggcggaactgtgtgcctcagcagatgcggcggttcagcgttgcagcgttggggcc 4156543
 QY 427 aggg 430
 Db 4156544 cggg 4156547

RESULT 10
 US-08-911-853-34
 ; Sequence 34, Application US/08911853
 ; Patent No. 6048710
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerritse, Gijbert
 ; APPLICANT: Quax, Wilhelmus J.
 ; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
 ; TITLE OF INVENTION: EXPRESSION LEVELS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genencor International
 ; STREET: 925 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1013
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/911,853
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/699,092
 FILING DATE: 16-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Glaister, Debra J
 REGISTRATION NUMBER: 33,888
 REFERENCE/DOCKET NUMBER: GC361-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-846-7620
 TELEFAX: 650-845-6504
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1176 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-911-853-34

Query Match 7.1%; Score 35; DB 3; Length 1176;
 Best Local Similarity 56.5%; Pred. No. 17;
 Matches 65; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 311 tggctgtgagcagctgacccctgcctgcacagcacaactctctctgtgtctgtg 370
 Db 1058 TGTCGCCGAGAGCGCGGCGGATCCGCGACACCTGTGCGCGGTGCGCGTGG 1117
 QY 371 accctgaacaggtgttcacgctcagctcagctgtctctgtgcccagctctgggtggct 425
 Db 1118 GCCTGGAAGACGTGTGACCTCAAGCGGACCTGGCCGCTGCGCGCTG 1172

RESULT 11
 US-09-479-409-34
 ; Sequence 34, Application US/09479409
 ; Patent No. 6225106
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerritse, Gijbert
 ; APPLICANT: Quax, Wilhelmus J.
 ; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
 ; TITLE OF INVENTION: EXPRESSION LEVELS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genencor International
 ; STREET: 925 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1013
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/479,409
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/911,853
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Glaister, Debra J
 ; REGISTRATION NUMBER: 33,888
 ; REFERENCE/DOCKET NUMBER: GC361-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-846-7620
 ; TELEFAX: 650-845-6504
 ; INFORMATION FOR SEQ ID NO: 34:

QY	371	acccTgaacagttTgcagcgTcaacgTcTccTggccacagctctTggcTgTgTcT	425
Db	1118	GCCTGGAGACGTGGTGCACCTCAAGGCGGACCTGGCCCGTGGCCTGGCCGCGCT	1172

RESULT 13

US-08-387-942C-20

Sequence 20, Application US/083879420
Patent No. 5939289
GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA

APPLICANT: SKAK-BRAEK GUDMUND
 APPLICANT: LARSEN BJORN
 TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
 TITLE OF INVENTION: ENCODING MANNONAN C-5-EPIMERASE
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP

RESULT 12

US-09-479-453-34
; Sequence 34, Application US/09479453

1 GENERAL INFORMATION:
2 APPLICANT: Gerltse, Gjsbert
3 APPLICANT: Onax, Wilhelmus J
4 TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
5 TITLE OF INVENTION: EXPRESSION LEVELS
6 NUMBER OF SEQUENCES: 37
7 CORRESPONDENCE ADDRESS:

ADDRESSSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/479,453
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
ATTORNEY NAME:

ATTORNEY/AGENT INFORMATION:
NAME: Glatster, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:

```

? TELEPHONE: 650-846-7620
? TELEFAX: 650-845-6504
? INFORMATION FOR SEQ ID NO: 34
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1176 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
US-09-479-453-34

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Query Match	7.18;	Score 35;	DB 4;	Length 1176;
Postcard of ...				
...				

Best Local Similarity	56.5%	Pred. No. 1.7;							
Matches	65;	Conservative	0;	Mismatches	50;	Indels	0;	Gaps	0;

QY		311	tgtgctgtgagcagactaacccctgccttcgacagcaaccaattcctgtgtgctcg	370
Db	1058	TGTCGGCGACAGAGCGGCCGATATCCGCACAACTGTGTCGCTGTGCGCCGTGG	1117	

```

QY 371 accccgaacaggtgtccagcgtcaacgtcgtccctggcccaagctctggtctggtc 425
    || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1118 GCCTGGAAAGACGTTGTCGACTCAAGGCCGACCTGGCCCGTGGCCCTGGCCGCGCT 117

```

RESULT 13
US-08-387-942C-20

Sequence 20, Application US/083879420
Patent No. 5939289
GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA

APPLICANT: SKAK-BRAEK GUDMUND
 APPLICANT: LARSEN BJORN
 TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
 TITLE OF INVENTION: ENCODING MANNONAN C-5-EPIMERASE
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP

STA

COUNTRY: USA
ZIP: 22042

```

1 MEDIUM TYPE: Floppy disk
2
3 COMPUTER: IBM PC compatible
4
5 OPERATING SYSTEM: PC-DOS/MS-DOS
6
7 SOFTWARE: PatentIn Release #1.0, Version #1.30
8
9 CURRENT APPLICATION DATA:
10
11 APPLICATION NUMBER: US/08/387,942C
12
13 FILING DATE: 03-MAY-1995

```

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: nucleic acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-942C-20

```

Query Match	7.18;	Score 34.8;	DB 2;	Length 1155;
Best Local Similarity	48.98;	Pred. No. 1.9;		
Matches 93;	Conservative	0;	Mismatches 97;	Indels 0;
			Gaps	0;

DQ 210 gctggagcaatgtgtccctcaattgagcaactcccagcgacgaactgtggaggagaccag 267
||| ||| | | |||| | | ||| ||| ||
Db 672 GCAGCGGCTCCTCCGACGTGGGCACCCTAAGACAATCCTGATTCGACGGCGGCCCTA 731

Oy 270 ccggaacgttgagagcaaggtacgcagcgtctgaaaggccctggfctgtagagcaagctgac 322
| | | | |
Db 732 ctacgacacaagcgcttggaaagcgctgacgatcaagaatggccaccagcgttcacctctgacagaa 791
| | | | |

QY 330 cccctgccttcacagcaccacaactctctcctgtgtgtgcgttggaccctgaacagtgltcca 385
 ---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
 792 CGCCGAGATCTACGGCAACGGCCTATACGSGGGTGGCCGCTCTACGGGCGCCGAGAGATGTCCA 851
 Db

Qy	390	gcgtcacg	tc	395
Db	852	GATCCTCGAC		861

RESULT 14

US-08-387-942C-1

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/ Sequence 1, Application US/08387942C
/ Patent No. 5939289
/ GENERAL INFORMATION:
/ APPLICANT: ERTESVAG, HELGA
/ APPLICANT: VALLA, SVEIN
/ APPLICANT: SKJAK-BRAEK, GUDMUND
/ APPLICANT: LARSEN, BJORN
/ TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
/ TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
/ STREET: P.O. BOX 747
/ CITY: FALLS CHURCH
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22042
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/387,942C
/ FILING DATE: 09-MAY-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MORPHY JR, GERALD M.
/ REGISTRATION NUMBER: 28,977
/ REFERENCE/DOCKET NUMBER: 1809-106P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-205-8000
/ TELEFAX: 703-205-8050
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12588 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ ORGANISM: Azotobacter vinelandii
/ STRAIN: E
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 290..1951
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 2227..6438
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 6702..9695
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 9973..12588
/ US-08-387-942C-1

Query Match          7.1%; Score 34.8; DB 2; Length 12588;
Best Local Similarity 48.9%; Pred. No. 3.8;
Matches 93; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
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QY 390 gcgtcacgtc 399
| | | |
Db 7553 GATCCTCGAC 7562

RESULT 15
US-08-387-942C-17
/ Sequence 17, Application US/08387942C
/ Patent No. 5939289
/ GENERAL INFORMATION:
/ APPLICANT: ERTESVAG, HELGA
/ APPLICANT: VALLA, SVEIN
/ APPLICANT: SKJAK-BRAEK, GUDMUND
/ APPLICANT: LARSEN, BJORN
/ TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
/ TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
/ STREET: P.O. BOX 747
/ CITY: FALLS CHURCH
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22042
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/387,942C
/ FILING DATE: 09-MAY-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MORPHY JR, GERALD M.
/ REGISTRATION NUMBER: 28,977
/ REFERENCE/DOCKET NUMBER: 1809-106P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-205-8000
/ TELEFAX: 703-205-8050
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1176 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-387-942C-17

Query Match          7.0%; Score 34.6; DB 2; Length 1176;
Best Local Similarity 50.9%; Pred. No. 2.2;
Matches 82; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
```

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QY 250 ctgtgtgaggagcaccagccgggaagctgtggaagcaggtacagctgtgcaagcc 309
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 712 CTGATCGACGGCGCGCTCTACTACGACACAGCCCGCAAGCGTGTCTTAAGATGACC 771

QY 310 ttggtgtgagcagctgacccctgtccctgtcacagcaccacacttctctgtgtcgtg 369
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 772 AGCGACATCAACCTTGCAAGACCGCGATATCCAGCAAGCGCTCTCCGGGCTCGGCTC 831

QY 370 gaccctgaacaagttgtccagcggtcacgtgtcgtgcccac 410
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 832 TACGGCGCCGACGAGCTGATCTCTGATTAACCAAGATCCA 872
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Search completed: August 19, 2002, 23:00:22
Job time: 4368 sec

OM of: US-09-786-130-1 to: GenEmbl:* out-format : pfs

Date: Aug 19, 2002 11:54 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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-O=/cgn2.1/USPTO_spool/US09786130/runat.15082002.160056.6297/app.query.fasta_1.222  
-Db=GenEmbl -QEMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.500  
-MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.500 -GAPOP=4.500  
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000  
-DELEXTE=7.000 -START=1 -MATRIX=blsum62 -TRANS=humand40 cdi  
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTPMT=pfs -NORM=ext -HEAPSIZ=500  
-MINLEN=0 -MAXLEN=200000000 -USER=US09786130.@cgnl.1_3896  
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMECUT=120 -WARN_TIMECUT=30  
-NO_XLPHY -WAIT -THREADS=1
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Search information block:

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Query: US-09-786-130-1  
Query Length: 164  
Database: GenEmbl:*  
Database sequences: 1797656  
Database length: 187333701  
Search time (sec): 1803.670000
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score_list:

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gb_pr:AB019504	+	870.00	1276.60	9.0e-63	585	AB019504 Homo sapiens mRNA for
gb_pat:E58840	+	870.00	1274.65	1.2e-62	744	E58840 Interleukin 18 binding F
gb_pat:AX005900	+	870.00	1269.82	2.3e-62	1348	AX005900 Sequence 1 from Paten
gb_pr:AF110799	+	870.00	1269.82	2.3e-62	1348	AF110799 Homo sapiens interl
gb_pr:AF122906	+	870.00	1269.78	2.3e-62	1355	AF122906 Homo sapiens MCS1L-53
gb_pr:AF110801	+	821.50	1190.58	5.9e-58	3630	AF110801 Homo sapiens interl
gb_pat:AX005904	+	821.50	1189.18	1.2e-57	7063	AX005904 Sequence 5 from Paten
gb_pat:E58837	+	727.00	1069.53	3.3e-51	411	E58837 Interleukin 18 binding F
gb_pr:AF122908	+	638.50	924.86	1.2e-42	7812	AF122908 Homo sapiens MCS1L-53
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gb_pr:AP002450	+	638.50	889.72	3.4e-41	19186	AP002450 Homo sapiens genom
gb_pr:AP000719	+	598.50	869.24	4.7e-40	1360	AP000719 Homo sapiens genom
gb_pat:AX005906	+	598.50	869.24	4.7e-40	1766	AX005906 Sequence 7 from Paten
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gb_pr:AF154569	+	523.00	763.93	3.5e-34	873	AF154569 Rattus norvegicus int
gb_ro:AF110803	+	523.00	760.64	5.3e-34	1310	AF110803 Mus musculus interl
gb_ro:BC018332	+	515.00	756.79	8.6e-34	495	BC018332 Mus musculus interl
gb_pat:E58836	+	515.00	756.48	1.0e-33	582	E58836 Interleukin 18 binding F
gb_ro:AB019505	+	515.00	752.43	1.5e-33	847	AB019505 Mus musculus mRNA for
gb_pat:E58844	+	515.00	748.23	2.6e-33	1422	E58844 Interleukin 18 binding F
gb_ro:AF122907	+	477.50	688.24	5.7e-30	2612	AF122907 Mus musculus MCS1L-53
gb_pat:E58841	+	441.00	650.95	6.8e-28	351	E58841 Interleukin 18 binding F
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gb_pat:AX005902	+	312.50	453.50	6.8e-17	1038	AX005902 Sequence 3 from Paten
gb_pr:AF110800	+	285.50	367.81	1.1e-12	88166	AF110800 Homo sapiens interl
gb_hlg:AC098760	+	244.00	365.03	5.7e-12	234	AC098760 Rattus norvegicus cl
gb_pat:E58839	+	217.00	317.01	2.7e-09	657	E58839 Interleukin 18 binding F
gb_v1:MC0271163	+	205.00	253.38	9.5e-06	120289	MC0271163 Molluscum contagiosu
gb_v1:MC060315	-	124.00	156.56	2.34	12518	MC060315 Molluscum contagiosu
gb_v1:AF335528	-	124.00	130.36	31.21	150773	AF335528 Lumpy skin disease v
gb_pr:HS1158812	-	119.00	136.68	64.67	122884	HS1158812 Lumpy skin disease
gb_v1:YD1293568	-	115.50	124.22	148.04	144575	YD1293568 Yaba-like disease v
gb_pr:AC002293	-	109.50	131.89	55.40	19000	AC002293 Genomic sequence frc
gb_pr:AC002102	-	109.50	131.89	55.40	44078	AC002102 Homo sapiens chromo
gb_hlg:AC010535	-	108.50	112.11	699.75	181233	AC010535 Homo sapiens chrom
gb_pr:AL137790	+	107.50	113.50	585.32	127409	AL137790 Human DNA sequence

gb_pr:AL145931	-	107.50	110.93	814.66	175033	AL145931 Human DNA sequen
gb_v1:AF380138	-	107.50	109.87	920.67	196858	AF380138 Monkeypox virus
gb_hlg:AC019225	-	107.50	109.82	939.03	200627	AC019225 Homo sapiens chr
gb_pat:AR145593	+	106.00	157.99	1.95	405	AR145593 Sequence 45 from p
gb_pat:158307	+	106.00	157.99	1.95	405	158307 Sequence 45 from pat

seq_name: gb_pat:E58835

seq_documentation block:

LOCUS	E58835	492 bp	DNA	linear	PAT 31-JAN-2002
DEFINITION	Interleukin 18 binding protein.				
ACCESSION	E58835				
VERSION	E58835.1 GI:18629908				
KEYWORDS	JP 2000210087-A/1.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 492)

Torikoshi, K., Tanai, M. and Kurimoto, M.

FEATURES	FT	Key	Location/Qualifiers
source	1..492	Location/Qualifiers	
BASE COUNT	97 a	171 c	136 g
ORIGIN	88 t		

alignment_scores:

Quality:	870.00	Length:	164
Ratio:	5.305	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

US-09-786-130-1 x E58835

Align seg 1/1 to: E58835 from: 1 to: 492

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1	ACACCTGCTCGCAGACACACACACCTGCTGCTAGTAGAGAC	50
17	TlAspProCysProSerGlnProProValPheProAlaAlaLysGlnC	34
51	AAAGGACCCCGCCCGCCCGCCCGCCCGCTGCCAGCCTGAAGCAGT	100
34	ysProAlaLeuGluValThrThrProGluValAlaGluValProLeuAsnGly	50
101	GTCACGACCTTGGAAGTGCCTGCGCCAGAGGTGGAAGTCCCTGAATGGA	150
51	ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSerI	67
151	ACGCTGAGCTTATCTGCTGCTGCTGCTGCTGCCAGCTGCCACCTTCAGCAT	200
67	eLeuTyrTrpLeuGlnLysnGlySerPheIleGluHisLeuProGlyArgL	84
201	CCTCTACGCTGCTGCGCAATGCTTCTTCATTCATGACACCTCCAGCGCCAGC	250

84 eutrpugllyserthrserargluarglyserthrgrglythrlnleu 100
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251 TGTGGAGGGGAGACACCGGGAACGTGGGAGACAGGTACGACAGCTG 300
101 CysLysAlaLeuValLeuGlnLeuThrProAlaLeuHisSerThrAs 117
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301 TGCAGAGCCTGTGCTGCTGGAGCAGCTGACCCCTGCTGGACAGCA 350
351 CTCTCTCTGTGCTGCTGGAGCAGCTGACCCCTGCTGGACAGCA 400
117 npheserCysValLeuValAspProGlnValValGlnArgHisValY 134
|||||
134 alleuAlaGlnLeuTrpAlaGlyLeuArgAlaThrLeuProProthrgln 150
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401 TCCTGGCCCAAGCTCTGGCTGGCTGAGGGCAACCTTGCCCCCACC 450
151 GluAlaLeuProSerSerHisSerSerProGlnGlnGly 164
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451 GAAGCCCTGCTCCAGCCACAGCAGTCCACAGCAGAGGCT 492

seq_name: gb_AB019504

seq_documentation_block:

LOCUS AB019504 585 bp mRNA linear PRI 31-MAR-1999
DEFINITION Homo sapiens mRNA for interleukin-18 binding protein, complete cds.
ACCESSION AB019504
VERSION AB019504.1 GI:4586394
KEYWORDS interleukin-18 binding protein.
SOURCE Homo sapiens (isolate:white) male liver cDNA to mRNA.
ORGANISM Homo sapiens

REFERENCE 1 (sites)
AUTHORS Alizawa,Y., Akita,K., Tanai,M., Korigoe,K., Mori,T., Nishida,Y.,
Ushio,S., Nukada,Y., Tanimoto,T., Ikegami,H., Ikeda,M. and
Kurimoto,M.

TITLE Cloning and expression of interleukin-18 binding protein
JOURNAL FEBS Lett. 445 (2-3), 338-342 (1999)

REFERENCE 2 (bases 1 to 585)
AUTHORS Alizawa,Y.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1998) Yasushi Alizawa, Hayashibara Biochemical
Laboratories, Inc., Fujisaki Institute, 675-1, Fujisaki, Okayama,
Okayama 702-8006, Japan (E-mail:Fujisaki@hayashibara.co.jp,
Tel:81-86-276-3141, Fax:81-86-276-6885)

COMMENT Sequence updated (30-Nov-1998).

FEATURES
Location/Qualifiers

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1..585

/codon_start=1

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RSTDRPSQPPVPPAKQCCPACALVETVPEVNPVPLNGTSLSCVACSRPNSILTWLS
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91..582

mat_peptide

/product="interleukin-18 binding protein"

BASE COUNT 116 a 203 c 157 g 109 t

ORIGIN

alignment_scores:
Quality: 870.00
Ratio: 5.305

Length: 164
Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-786-130-1 x AB019504 ..

Align seg 1/1 to: AB019504 from: 1 to: 585

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17 rlyAspProCysProSerGlnProProValPheProAlaAlaLysGlnC 34
|||||
141 AAAGGACCCCTGCTCCCTCCAGCCCAAGTTCCTCCAGCAGTTAACAGT 190
34 ySProAlaLeuGluValThrTrpProGlnValGluValProLeuAsnGly 50
|||||
191 GTCCACGATTTGGAAGTACCTGGCCAGAGGTGGAAGTGCACATGATGCA 240
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheser11 67
|||||
241 ACCGTGAGCTTATCTGTGTGGCTGACGCGCTTCCCAACTTCAGCAT 290
67 eleuTyrrTrpLeuGlyAsnGlySerPheTleGluHisLeuProGlyArgL 84
|||||
291 CCTCTACTGCTGGCAATGGTTCCTCATTTGAGCAGCTCCAGGCCGAC 340
84 eutrpugllyserthrserargluarglyserthrgrglythrlnleu 100
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341 TGTGGAGGGGAGACACCAGCCGGGAACGTGGAGACAGGTACGACAGCTG 390
101 CysLysAlaLeuValLeuGlnLeuThrProAlaLeuHisSerThrAs 117
|||||
391 TGCAGAGCCTGTGCTGCTGGAGCAGTGCACCCCTGCTGCACAGCACA 440
117 npheserCysValLeuValAspProGlnValValGlnArgHisValY 134
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441 CTCTCTCTGTGCTGCTGGAGCCTGACAGGTTGTCAAGCGCAGAGCTG 490
134 alleuAlaGlnLeuTrpAlaGlyLeuArgAlaThrLeuProProthrgln 150
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491 TCCTGGCCCAAGCTCTGGCTGGCTGAGGGCAACCTTGCCCCCACC 540
151 GluAlaLeuProSerSerHisSerSerProGlnGlnGly 164
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seq_documentation_block:

LOCUS E58840 744 bp DNA linear PAT 31-JAN-2002

DEFINITION Interleukin 18 binding protein.

ACCESSION E58840

VERSION E58840.1 GI:18629913

KEYWORDS JP 2000210087-A/6.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 744)
AUTHORS Torikoshi,K., Tanai,M. and Kurimoto,M.
TITLE Interleukin 18 binding protein
JOURNAL Patent: JP 2000210087-A 6 02-AUG-2000;
HAYASHIBARA BIOCHEM LAB INC

COMMENT OS Homo sapiens (human)
PN JP 2000210087-A/6
PD 02-AUG-2000
PF 28-MAY-1999 JP 1999149498
PR KAKUI TORIKOSHI,MADOKA TANAI,MASASHI KURIMOTO PC
C12N15/09,A61K31/00,A61K38/00,A61K39/395,C07K14/47,C07K14/715,PC
C07K16/18//
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/db_xref="taxon:9606"

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ORIGIN

alignment_scores:

Quality: 870.00 Length: 164
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-786-130-1 x E58840 ..

Align seg 1/1 to: E58840 from: 1 to: 744

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34 ySProAlaLeuGluValThrTPrProGluValGluValProLeuAsnGly 50
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260 GTCCAGCATTTGGAAGTGACCTGGCCAGAGGTGGAAATGCCCATGAATGA 309
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51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSerI 67
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310 ACGCTGAGCTTATCCTGCTGTGGCTGCAGCCGCTCCCAACTTCACCAT 359
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67 eLeuTyTTrpLeuGlyAsnGlySerPheIleGluHisLeuProGlyArgL 84
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360 CCTTACTGCTGGGCAATGGTTCTTCATTGACACCTCCACAGGCGGAC 409
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84 eutPrpGluGlySerThrSerArgGluArgGlySerThrGlyThrGlnLeu 100
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410 TGTGGAGGGGAGACACACCGGGAGACGTGGAGACACAGGTACGCACTG 459
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101 CysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThrAs 117
|||||
460 TGCAGGCTTGTGGTGTGGAGACAGTGAACCTGCTCCGACACAGCAACAA 509
|||||
117 nPheSerCysValLeuValAspProGluGlnValAlaGlnArgHisValY 134
|||||
510 CTTCCTCTGTGTGCTGTGGACCTGTGAACAGTTGTCCAGCGTACGCTCG 559
|||||
134 alaLeuAlaGlnLeuTrpAlaGlyLeuArgAlaThrLeuProProThrGln 150
|||||
560 TCCGAGCCAGCTCTGGGCTGGGCTGAGGGCAACCTGCCCCCACCACCA 609
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610 GAAGCCCTGCCCTCCAGCACACAGCATGCCAGCAGCAGAGGT 651
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seq_name: gb_pat:AX005900

seq_documentation_block:

LOCUS AX005900 1348 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 1 from Patent WO9909063.
ACCESSION AX005900
VERSION AX005900.1 GI:9928886
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 1348)
AUTHORS RubinsteiN,M. and Kim,S.H.
TITLE Interleukin-18 binding proteins, their preparation and use
JOURNAL Patent: WO 9909063-A 1 25-FEB-1999.
RUBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)
FEATURES Location/Qualifiers
source 1..1348
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BASE COUNT 304 a 449 c 292 g 303 t
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Quality: 870.00 Length: 164
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

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17 rLyAspProCysProSerGlnProProValPheProAlaAlaLysGlnC 34
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200 AAAGGACCCCTGCCCTCCAGCCCGAGTGTCCAGCAGCTAAAGCAGT 249
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34 ySProAlaLeuGluValThrTPrProGluValGluValProLeuAsnGly 50
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51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSerI 67
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67 eLeuTyTTrpLeuGlyAsnGlySerPheIleGluHisLeuProGlyArgL 84
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seq_name: gb_pt:AF110799

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LOCUS AF110799 1348 bp mRNA linear PRI 03-MAR-1999
DEFINITION Homo sapiens interleukin-18 binding protein a precursor (IL18BP)
ACCESSION AF110799
VERSION AF110799.1 GI:4324927
KEYWORDS mRNA, complete cds.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1348)
AUTHORS Novick,D., Kim,S.H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A. and
Rubinstein,M.
TITLE Interleukin-18 binding protein: a novel modulator of the Th1
cytokine response
JOURNAL Immunity 10 (1), 127-136 (1999)
MEDLINE 99146382
REFERENCE 2 (bases 1 to 1348)
AUTHORS Novick,D., Kim,S.H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A.
and Rubinstein,M.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-1998) Molecular Genetics, Weizmann Institute of
Science, P.O. Box 26, Rehovot 76100, Israel
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BASE COUNT 304 a 449 c 292 g 303 t
ORIGIN
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Quality: 870.00 Length: 164
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Percent Similarity: 100.000 Percent Identity: 100.000
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US-09-786-130-1 x AF110799 ..
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LOCUS AF122906 1355 bp mRNA linear PRI 28-JUN-1999
DEFINITION Homo sapiens MC51L-53L-54L homolog mRNA, complete cds.
ACCESSION AF122906
VERSION AF122906.1 GI:5231015
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1355)
AUTHORS Xiang,Y. and Moss,B.
TITLE Identification of human and mouse homologs of the MC51L-53L-54L
family of secreted glycoproteins encoded by the Molluscum
contagiosum poxvirus
JOURNAL Virology 257 (2), 297-302 (1999)
MEDLINE 99263157
PUBMED 10329540
REFERENCE 2 (bases 1 to 1355)
AUTHORS Xiang,Y. and Moss,B.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-1999) NIAID/LVD, NIH, 9000 Rockville Pike,
Bethesda, MD 20892, USA
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BASE COUNT 293 a 455 c 298 g 309 t
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Ratio: 5.305 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000
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Align seg 1/1 to: AF122906 from: 1 to: 1355.

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219 AAAGACCCCTGCCCTGCCAGCCCCCAGTGTCCAGACAGTAAAGCAGT 268
34  ysProAlaLeuGluValThrTTPProGluValGluValProLeuAsnGly 50
|||||
269 GTCCAGCATTTGGAGTAGTACCTGGCCAGAGGTGGAAAGTGCCTGAATGA 318
51  ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheserIl 67
|||||
319 ACCTGAGCTTATCTGTGTGCTGCAGCCGCTTCCCACTTCAGCAT 368
67  eLeuTyrTrpLeuGlyAsnGlySerPheIlleGluHisLeuProGlyArgL 84
|||||
369 CCTCTACTGGCTGGGCAATGGTCTTCATTCATGACACCTCCAGCGCCAG 418
84  eutTpgGluGlySerThrSerArgGluArgGlySerThrnglyThGlnLeu 100
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419 TGTGGAGGGGAGACACACCGGAGACGTGGAGACACAGTACCCACTGT 468
101 CysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThrAs 117
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469 TGCAGAGCCTTGTGCTGAGACAGCTACCCCTCCCTGCACAGACACAA 518
117 nPheSerCysValLeuValAspProGluGlnValGlnArgHisValY 134
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519 CTCTCTCTGTGTGCTGCTGAGACCTGGAACAGGTGTCCAGCGTCACTGC 568
134 alleuAlaGlnLeuTrpAlaGlyLeuArgAlaThrLeuProProthGln 150
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569 TCCGTGGCCAGCCTCTGGCTGGCTGAGGGCAACCTTGCCCCCAACCCAA 618
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seq_name: gb_pr:AF110801

seq_documentation_block:

LOCUS AF110801 3630 bp mRNA linear PRI 03-MAR-1999
DEFINITION Homo sapiens interleukin-18 binding protein c precursor (IL18BP)
MRNA, complete cds.

ACCESSION AF110801 GI:4324931

VERSION AF110801

KEYWORDS

SOURCE

ORGANISM

human.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (04-DEC-1998) Molecular Genetics, Weizmann Institute of
Science, P.O. Box 26, Rehovot 76100, Israel

FEATURES
source Location/Qualifiers

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929..1522
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929..1012

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mat_peptide

BASE COUNT 834 a 1022 c 995 g 779 t
ORIGIN

alignment_scores:

Quality: 821.50 Length: 241
Ratio: 5.009 Gaps: 1
Percent Similarity: 68.050 Percent Identity: 68.050

alignment_block:

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seq_documentation_block:

LOCUS AX005904 7063 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 5 from Patent WO9909063.
ACCESSION AX005904
VERSION AX005904.1 GI:9928888
KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 7063)

AUTHORS Rubinstein,M. and Kim,S.H.

TITLE Interleukin-18 binding proteins, their preparation and use

JOURNAL Patent: WO 9909063-A 5 25-FEB-1999;

RUBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)

FEATURES Location/Qualifiers

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/db_xref="taxon:9606"

BASE COUNT 1538 a 2025 c 1981 g 1519 t

ORIGIN

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Quality: 821.50 Length: 241
Ratio: 5.009 Gaps: 1
Percent Similarity: 68.050 Percent Identity: 68.050

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seq_documentation_block:

LOCUS E58837 411 bp DNA linear PAT 31-JAN-2002
DEFINITION Interleukin 18 binding protein.
ACCESSION E58837
VERSION E58837.1 GI:18629910
KEYWORDS JP 2000210087-A/3.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 411)

AUTHORS Torikoshi,K., Tanai,M. and Kurimoto,M.

TITLE Interleukin 18 binding protein

JOURNAL Patent: JP 2000210087-A 3 02-AUG-2000;

HAYASHIBARA BIOCHEM LAB INC

OS Homo sapiens (human)

PN JP 2000210087-A/3

PD 02-AUG-2000

PF 28-MAY-1999 JP 1999149498

PR KAKUJI TORIKOSHI,MADOKA TANAI,MASASHI KURIMOTO PC

C12N15/09,A61K31/00,A61K38/00,A61K39/395,C07K14/47,C07K14/715, PC

C07K16/18//

PC C12P21/08,C12N15/00,A61K37/02

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CC      Key      Location/Qualifiers
FH      source      1. 411
FT      Location/Qualifiers
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DEFINITION Homo sapiens MC51L-53L-54L homolog gene, partial cds.
ACCESSION      AF122908
VERSION      AF122908.1 GI:5231019
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 2528)
AUTHORS      Xiang,Y. and Moss,B.
TITLE      Identification of human and mouse homologs of the MC51L-53L-54L

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JOURNAL      family of secreted glycoproteins encoded by the Mollicum
MEDLINE      contagiosum poxvirus
PUBMED      virology 257 (2), 297-302 (1999)
REFERENCE      2 (bases 1 to 2528)
AUTHORS      Xiang,Y. and Moss,B.
TITLE      Direct Submission
JOURNAL      Submitted (25-JAN-1999) NIAID/LVD, NIH, 9000 Rockville Pike,
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431  GTTACCTCTGAGGCGCAGTCCCTTCTGGCCCATGTACACACAGCTGAGC 480
48  .....
481  CAGCTGGGTGAGCAGCAGCATTCCTCCTCCCAACCAAGTGTCAATGGG 530
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731 AGTCACGAGAGCTGGGCACTAGAAAAGTCACTCTGAGAGACAGTTCA 780
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781 GAAGAGATTTCATACGTGAACCAAGGACATTCCTACATTCGCCGTGT 830
48 ..... 48
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48 ..... 48
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LOCUS AX005908 7812 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 9 from Patent WO9909063.
ACCESSION AX005908
VERSION AX005908.1 GI:9928890
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 7812)
AUTHORS Rubinstein,M. and Kim,S.H.
JOURNAL Interleukin-18 binding proteins, their preparation and use
Patent: WO 9909063-A 9 25-FEB-1999;
RUBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)
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/db_xref="taxon:9606"
BASE COUNT 1689 a 2278 c 2167 g 1678 t
ORIGIN

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Quality: 638.50 Length: 483
Ratio: 3.893 Gaps: 5
Percent Similarity: 33.954 Percent Identity: 33.540

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seq_name: gb_pr:AF110798

seq_documentation_block:
LOCUS AF110798 8292 bp DNA linear PRI 03-MAR-1999
DEFINITION Homo sapiens interleukin-18 binding protein precursor (IL18BP)
ACCESSION AF110798
VERSION AF110798.1 GI:4324923
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 8292)
Novick,D., Kim,S.H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A. and
Rubinstein,M.
Interleukin-18 binding protein: a novel modulator of the Th1
cytokine response
Immunity 10 (1), 127-136 (1999)
2 (bases 1 to 8292)
Novick,D., Kim,S.-H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A.
and Rubinstein,M.
Direct Submission
Submitted (04-DEC-1998) Molecular Genetics, Weizmann Institute of
Science, P.O. Box 26, Rehovot 76100, Israel
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sequence.
ACCESSION AP002490
VERSION AP002490.4 GI:15637090
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 191986)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
2 (bases 1 to 191986)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Sep 17, 2001 this sequence version replaced gi:15617455.
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DEFINITION Homo sapiens genomic DNA, chromosome 11q clone:RP11-757C15,
complete sequences.
ACCESSION  AP000719
VERSION    AP000719.4  GI:13094220
KEYWORDS   HTG.
SOURCE      Homo sapiens DNA, clone:RP11-757C15.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (sites)
AUTHORS    Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
            Homo sapiens genomic DNA
            Published Only in DataBase (1999) In press
            2 (bases 1 to 196424)
            Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
            Direct Submission
            Submitted (11-NOV-1999) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
            1-7-22 Suehiro-chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
            Tel:81-45-503-9111, Fax:81-45-503-9170)
            On Feb 21, 2001 this sequence version replaced gi:9927288.
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VERSION AX005906.1 GI:9928889
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1360)
REFERENCE Rubinstein, M. and Kim, S.H.
AUTHORS Interleukin-18 binding proteins, their preparation and use
TITLE Patent: WO 9909063-A 7 25-FEB-1999;
JOURNAL RUBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)

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About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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AC AAAI1002;

DT 28-JUL-2000 (first entry)

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KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;

KW regulator; drug; sensitivity disease; organ rejection; organ transplant;

KW autoimmune disease; ss.

OS Homo sapiens.

PN WO200012555-A1.

PD 09-MAR-2000.

PE 18-NOV-1998; 98WO-JP05186.

XX 01-SEP-1998; 98JP-0247588.

PR 18-NOV-1998; 98JP-0327914.

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PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PT Toriigoe K, Tanai M, Kurimoto M;

DR WPI; 2000-237850/20.

XX P-PADB; AAY83951.

PT Interleukin 18-binding protein with activity of regulating

PT physiological actions of interleukin 18, useful as regulator and drug

CC for sensitivity diseases and organ rejection and in treating diseases

CC due to excess immune reaction -

PS Claim 6; Page 57-59; 71pp: Japanese.

CC The invention relates to novel interleukin 18 (IL-18)-binding proteins

CC from humans or mice which act as regulators and drugs for sensitivity

CC diseases and organ rejection and in treating diseases due to excess

CC immune reaction, e.g. in slowing down rejection after organ transplant,

CC and in treating autoimmune diseases. This sequence represents the coding

CC sequence for the mature human interleukin 12 binding protein.

SQ Sequence 492 BP; 97 A; 171 C; 136 G; 88 T; 0 other;

alignment_scores:

Alignment	Quality	Ratio	Length
US-09-786-130-1 x AAAI1002	870.00	5.305	164
Percent Similarity: 100.000	Percent Identity: 100.000		0

Align seg 1/1 to: AAAI1002 from: 1 to: 492

1 ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerTh 17
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1 ACACCTGCTCTGCAGACACACACAGCTGCCCTGCTAGTAAAGCAC 50
|||||
17 TlysAspProCysProSerGlnProProValPheProAlaAlaLysGlnC 34
|||||
51 AAAGGACCCCTGCCCCCTCCAGCCCCCAGTGTCCACAGCAGCTAAGCAGT 100
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34 ysfProAlaLeuGIuVal1ThrTTPProGIuVal1GluVal1ProLeuAsnGly 50
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101 GTCCACCATTTGGAAGTACCTGGCCAGAGGTGGAAGTGCACATGAATGGA 150
51 ThrluSerleuSerCysValAlaCysSerArgPheProAsnSerIle 67
   |||||||
151 AGCTGAGCTTATCTGTGTGGCTGCAGCCGCTCCCAACTTCAGCAT 200
67 eLeuTyrTrpLeuGIyAsnGIySerPheIleGIuHisIleuProGIyArgL 84
   |||||||
201 CCTCTACTGGCTGGCCATGGTCTTCATTATGACACCTCCAGGGCCGAC 250
84 eutPrluGIySerThrSerArgGIuArgGIySerThrGIyThrGIuLeu 100
   |||||||
251 TGTGGAGAGGGAGACACACCGGGAACGTGGGAGCACAGGTACGACGCTG 300
101 CysLysAlaLeuValLeuGIuGIuInleuThrProAlaLeuHisSerThrAs 117
   |||||||
301 TGCAGAGCCTTGGTGTGGAGCAGCTGACCCCTGCTGCACACCCAA 350
117 nPheSerCysValLeuValAspProGIuGIuValAlaGIuArgHisValY 134
   |||||||
351 CTCTCTCTGTGTGTGGTGGACCTGAACAGGTGTCCAGCGTCACGTCG 400
134 allEuAlaGIuInleuTrpAlaGIyLeuArgAlaThrleuProProthrgIn 150
   |||||||
401 TCTGTGCCAGGCTGTGGCTGGGCTGAGGGCAACTTGCCTCCACCCAA 450
151 GIuAlaLeuProSerSerHisSerSerProGIuInGIuGIy 164
   |||||||
451 GAAGCCCTGCTCCAGCCACACAGTCCACAGCAGCAGAGGT 492

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAA11007
seq_documentation_block:
ID AAA11007 standard; DNA; 744 BP.
XX
AC AAA11007;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human interleukin 18 binding protein complete coding sequence.
XX
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW Regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease; ds.
XX
OS Homo sapiens.
XX
FH key Location/Qualifiers
FT CDS 70..654
FT /*tag= a
FT /product= "IL-18 binding protein"
FT sig_peptide 70..159
FT /*tag= b
FT mat_peptide 160..651
FT /*tag= c
XX
PN WO200012555-A1.
XX
PD 09-MAR-2000.
XX
PF 18-NOV-1998; 98WO-JP05186.
XX
PR 01-SEP-1998; 98JP-0247588.
XX
PR 18-NOV-1998; 98JP-0327914.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Torigoe K, Taniai M, Kurimoto M;
XX
DR WPI; 2000-237850/20.
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DR P-PSDB; AAY83985.
XX
PT Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction
XX
PS Example 2; Page 63-64; 71pp; Japanese.
XX
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the coding
CC sequence for the full length human interleukin 12 binding protein.
XX
SO Sequence 744 BP; 156 A; 249 C; 199 G; 140 T; 0 other:

alignment_scores:
Quality: 870.00 Length: 164
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-786-130-1 x AAA11007 ..
Align seg 1/1 to: AAA11007 from: 1 to: 744

1 ThrlProValSerGIuInleuThrTrpAlaAlaThrAlaSerValArgSerTh 17
   |||||||
160 ACACGTGTCTCGCAGACACACACAGCTGCCACGTGCTCGATTGAAGAC 209
17 rlyAspProCysProSerGIuProProValPheProAlaAlaLysGIu 34
   |||||||
210 AAGAGACCCCTGGCCCTCCAGGCCAGTGTTCACAGCAGCAACAGT 259
34 ysfProAlaLeuGIuVal1ThrTTPProGIuVal1GluVal1ProLeuAsnGly 50
   |||||||
260 GTCCACCATTTGGAAGTACCTGGCCAGAGGTGGAAGTGCACATGAATGGA 309
260 ThrluSerleuSerCysValAlaCysSerArgPheProAsnSerIle 67
   |||||||
310 AGCTGAGCTTATCTGTGTGGCTGCAGCCGCTCCCAACTTCAGCAT 359
67 eLeuTyrTrpLeuGIyAsnGIySerPheIleGIuHisIleuProGIyArgL 84
   |||||||
360 CCTCTACTGGCTGGCCATGGTCTTCATTATGACACCTCCAGCGTCGAC 409
84 eutPrluGIySerThrSerArgGIuArgGIySerThrGIyThrGIuLeu 100
   |||||||
410 TGTGGAGAGGGAGACACACCGGGAACGTGGGAGCACAGGTACGCGCTG 459
410 CysLysAlaLeuValLeuGIuGIuInleuThrProAlaLeuHisSerThrAs 117
   |||||||
101 CysLysAlaLeuValLeuGIuGIuInleuThrProAlaLeuHisSerThrAs 117
   |||||||
460 TGCAGAGCCTTGGTGTGGAGCAGCTGACCCCTGCTGCACACCCAA 509
560 nPheSerCysValLeuValAspProGIuGIuValAlaGIuArgHisValY 134
   |||||||
510 CTCTCTCTGTGTGTGGTGGACCTGAACAGGTGTCCAGCGTCACGTCG 559
134 allEuAlaGIuInleuTrpAlaGIyLeuArgAlaThrleuProProthrgIn 150
   |||||||
560 TCTGTGCCAGGCTGTGGCTGGGCTGAGGGCAACTTGCCTCCACCCAA 609
151 GIuAlaLeuProSerSerHisSerSerProGIuInGIuGIy 164
   |||||||
610 GAAGCCCTGCTCCAGCCACACAGTCCACAGCAGCAGAGGT 651

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:AAx24749
seq_documentation_block:
ID AAx24749 standard; CDNA; 1348 BP.
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XX The present sequence represents a cDNA clone coding for a human
CC interleukin-18 binding protein (IL-18BP) splice variant designated
CC IL-18Bpc (see AAM98005). This is one of 4 novel splice variants (see
CC AAM24749-52), all coding for putative soluble proteins (see
CC AAM98004-07), that were detected following a screening of human
CC peripheral blood monocyte, Jurkat T-cell, peripheral blood
CC mononuclear cell and spleen cell cDNA libraries using a probe
CC produced using IL-18BP-specific primers. IL-18Bpc is a low
CC abundance splice variant. IL-18BP polypeptides capable of
CC binding IL-18 and/or modulating and/or blocking IL-18 activity are
CC provided. Methods for their isolation and recombinant production,
CC DNA vectors expressing them, vectors useful for their expression in
CC humans and other mammals, and antibodies against them are also
CC provided. IL-18BP polypeptides, and DNA encoding them, can be used
CC to treat conditions requiring the protein (claimed). Conditions
CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,
CC graft rejections, inflammatory bowel disease, sepsis, multiple
CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic
CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
CC also useful for purifying IL-18 (claimed).

Sequence 7063 BP; 1538 A; 2025 C; 1981 G; 1519 T; 0 other;

alignment_scores:

Quality: 821.50 Length: 241

Ratio:	5.009	Gaps:	1
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Similarity: 68.050 Percent Identity: 68.050

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alignment_block:
US-09-786-130-1 x AAX24751 . .
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Align seg 1/1 to: AAX24751 from: 1 to: 7063

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17 rLysAspProCysProSerGlnProProValPheProAlaAlaLysLnc 34
|||||
1083 AAAGGACCCCTGCCTCCACAGCCCCCAGTGTTCCACAGCAAGTAAGAGT 1132
34 ysProAlaLeuGlnValThrTyrProGlnValGlnValProLeuAsnGly 50
|||||
1133 GTCCAGCATTTGGAAGAGCACTGGCCAGAGGTGAAGTGAAGCCATGAAGA 1182
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSerI 67
|||||
1183 ACGCTGAGCTTATCCCTGCTGGCTGCACCCGCTTCCCAACTTCACCAT 1232
67 eleuYrTrPLeuGlyAsnGlySerPheIleGlnHisLeuProGlyArgL 84
|||||
1233 CCTCTACTGTGGCTGGGCAATGGTTCTTCAATTGAGCACTCCAGGCCGAC 1282
84 eutRPluGlySerThrSerArgGluArgGlySerThrGlyThrGlnLeu 100
|||||
1283 TGTGGAGAGGGAGACACCAACCCGGGAACGTGGAGACACAGGTACGACACTG 1332
101 CysLysAlaLeuValLeuGlnGlnLeuThrProAlaLeuHisSerThrAs 117
|||||
1333 TGCAGAGCCCTTGCTGCTGGAGACAGCTGACCCCTGCCTGCACAGACCAA 1382
117 nPheSerCysValLeuValAspProGlnGlnValValAlaGlnArgHisValY 134
|||||
1383 CTTTCCTGTGTGTCTGTGGACCCCTGAACAGGTGTTCACACGTCACAGCTCG 1432
134 alleuAlaGlnLeuTrp..... 139
|||||
1433 TCCTGTGCCACGCTGTGGTGTGAGAGACCCCAAGAGAGAGCCTCCAGAGAACAG 1482
139 139

1483 GAGGACCTCTGCTTCATATGTGGGGGAGAAAGGTGGGCTCTGCCAG 1532
139 139

1533 CAGCCTGTGAATAATGCCAGCATTCCTCAAGSTCAGCAGACAAAG 1582
139 139

1583 GAACTTAAGTCTTGGGCGAGAGAGGTGTACCTGGGGCAAGATGATGGA 1632
140 A1 140

1633 TGTCCCTCTTCCTTGGCCGTATCCTGTGTGCCCTTCACTTCCCTAGGC 1682

140 aclyleuArGAlaThrLeuProPProThrIngluAlaLeuProSerSerH 157
|||||
1683 TGGGCGTAGGGGCAACCTTGGCCCCCAACCCAAAGAGCCCTGCCCTCAGCC 1732
157 lssSerSerProGInglInglInglly 164
|||||
1733 ACAGCAGTCCACGACGACAGGGT 1755

seq_name: /SIDS1/gcgydata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAA11004

seq_documentation_block:

ID AAA11004 standard; DNA; 411 BP.

AC AAA11004;

DT 28-JUL-2000 (first entry)

DE Human IL-18 binding protein 5' RACE fragment #1.

KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease; rapid amplification of cDNA ends; RACE; ss.

05 Homo sapiens.

FH	Key	Location/Qualifiers
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FT / *tag=

FT /note= "fragment of N-terminus of IL-18 binding protein"

PN W0200012555-A1.

PD 09-MAR-2000.

18-NOV-1998; 98WO-JP05186.

PR 18-NOV-1998; 98JP-0327914.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Toriqué K, Taniai M, Kurimoto M;

WPT: 2000-237850/20.

XX
E EDD, HALLS.

PT physiological activity

PT due to excess immune reaction in treating diseases for sensitivity and organ rejection and in treating diseases

Example 2: Page 60-61: 71nn: Japanese
XX
PS

CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC for humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the initial
CC


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48 ..... 48
1305 GTTACTCTGAGCGCAGTCCCTTGTGCCAATGTACCAACCACTGAGC 1354
48 ..... 48
1355 CAGCTGGGCTGAGCAGCAGCACTTCTCCCTCCCAACCACTGTATGGG 1404
48 ..... 48
1405 TGCAGGCTTGGCGAGCTCCCAAGATGCTCCCTATCAATAGACAGAGA 1454
48 ..... 48
1455 ACTAAGACATAGTAATGTGTACAGAGACTCCAGAGCCTTGGTTGCAG 1504
48 ..... 48
1505 TGAACCCCAAGGCGAGCCCTCCACCAAGAGCTGTGGCCTTGGCCAT 1554
48 ..... 48
1555 CTCAGAGAGCAGCAGCAGCATCCAGCAGCTGCTGTACCTGGGCTCCA 1604
48 ..... 48
1605 AGTACCGAGGCTGGCAGCTAGAAAAGTCTATCTGAGGAGACAGTTCA 1654
48 ..... 48
1655 GAAGAGATTATCATCGTAGAACCAAGACATTCCTCATTCCCGGTGT 1704
48 ..... 48
1705 TTAAGGCTAGGGCCTCTGGAGACACTGCATCTGTATACGGAGCTTCC 1754
48 ..... 48
1755 CACCTAGTGTGTGCAGAGCAGATTCTCTAGTTCCAGATCATGGGAC 1804
48 ..... 48
1805 TGGGGGAGCTGGCAGAGAGGACAGCAGAGCAGAGGTAAGGGGCC 1854
49 ..... Asn..GlyThrLeu 53
1855 TGCTCTTCTGAAGAGCTAACTGCTGCTGTGTCCTAGATGGAAAGCTGA 1904
53 erLeuSerCysValAlaCysSerArpPheProAsnPheSerIleLeuTyr 69
1905 GCTTATCTGTGTGGCTGCAGCGGCTTCCCACTTCAGATCTCTCTAC 1954
70 TrpLeuGlnAsnGlySerPheIleGlnHisLeuProGlyArgLeuTrpG1 86
1955 TGCGTGGGCAATGCTCTTCATTGAGCACCCTCCAGGCGCAGCTGTGGA 2004
86 uGly..... 87
2005 GGGGAGCAGCAGGTGAGGCTGCGCAGACCAAGTGGGTGGAGAAAGCC 2054
88 ..... Ser..ThrSerArgLys 93
2055 TTCTGGGCGCTTCTCATGACCTTTCCTCCCTCCGCTCCAGCGGGAAC 2104
93 rglGlySerThrGlyThrGlnLeuCysLysAlaLeuValLeuGlnLeu 109
2105 GTGGGAGCAGAGGTACGAGCTGTGCAAGGCTTGGTGTGAGACACTG 2154
110 ThrProAlaLeuHisSerThrAsnPheSerCysValLeuValaLapProG1 126
2155 ACCCTGCGCTGCGACAGACCAACTTCTCTGTGTCTGTGAGACCTGA 2204
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126 uGlnValValGlnArgHisValValLeuAlaGlnLeuTrp..... 139
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2205 ACAGGTTGTCCAGCGCTCAGCTGTCTCTGCGCCAGCTGTGGGAGAGACC 2254
139 ..... 139
2255 CAAGAGAGGCGCTCCAGAGACAGAGAGAGCTGTGCTTCATATGTGGGGA 2304
139 ..... 139
2305 GGAAGGCTGGGCTCTGCCAGAGCAGCCTGTGAATGATGCCACATTC 2354
139 ..... 139
2355 CTCAGGTACACACACAAAAAGACTTAGTCTTGGGCGAGAGAGGTG 2404
139 ..... 139
2405 TAGCCTGGGCAAGTGTATGAGATGTCCCTTCTTGGCGTATCCT 2454
140 ..... AlaglyLeuArgAlaThrLeuProProth 149
2455 TGCTGCTTGCATCTTCCCTAGGCTGGGCTGAGGCAACCTTGGCCCGAC 2504
149 rGlnGlnAlaLeuProSerSerHisSerSerProGlnGlnGly 164
|||||
2505 CCAAGAAAGCCCTGCGCTCCAGCCACAGCAGTCCACAGCAGCAGGCT 2550

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseq-n-emb1/NA1999.DAT: AAX24752
seq_documentation_block:
ID AAX24752 standard; cDNA; 1360 BP.
XX
AC AAX24752;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human Interleukin-18 binding protein splice variant IL-18Bpd cDNA.
XX
KW Interleukin-18 binding protein; IL-18BP; IL-18Bpd; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
KW ischemic heart disease; ischemic brain injury; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 169..654
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FT sig_peptide 169..252
FT FT /*tag= b
FT mat_peptide 253..651
FT FT /*tag= c
XX
PN MO9909063-A1.
XX
PD 25-FEB-1999.
XX
PF 13-AUG-1998; 98WO-IL00379.
XX
PR 22-JUL-1998; 98IL-0125463.
PR 14-AUG-1997; 97IL-0121554.
PR 27-AUG-1997; 97IL-0121639.
PR 29-SEP-1997; 97IL-0121860.
PR 06-NOV-1997; 97IL-0122134.
XX
PA (YEDA ) YEDA RES & DEV CO LTD.
XX
PI dinarello C, kim SH, Novick D, Rubinstein M;
XX
WP1; 1999-180975/15.
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DR P-PSDB; AAW98007.

PT New interleukin-18 binding protein - useful for treating human
 PT diseases, including autoimmune disease and inflammation
 XX
 XX
 Claim 12: Page 59; 100pp; English.
 PS
 XX

Claim 12; Page 59; 100pp; English.

The present sequence represents a cDNA clone coding for a human interleukin-18 binding protein (IL-18BP) splice variant designated CC IL-18BP (see AM96007). This is one of 4 novel splice variants (see AMX24749-52), all coding for putative soluble proteins (see AM968004-07), that were detected for putative screening of human peripheral blood monocyte, Jurkat T-cell, peripheral blood mononuclear cell and spleen cell cDNA libraries using a probe produced using IL-18BP-specific primers. IL-18BP is a low abundance splice variant. IL-18BP polypeptides capable of binding IL-18 and/or modulating and/or blocking IL-18 activity are provided. Methods for their isolation and recombinant production, DNA vectors expressing them, vectors useful for their expression in humans and other mammals, and antipeptides against them are also provided. IL-18BP polypeptides, and DNA encoding them, can be used to treat conditions requiring the protein (claimed). Conditions include autoimmune diseases, type I diabetes, rheumatoid arthritis, graft rejections, inflammatory bowel disease, sepsis, multiple sclerosis, ischemic heart diseases, ischemic brain injury, chronic hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is also useful for purifying IL-18 (claimed).

SQ Sequence 1360 BP; 289 A; 454 C; 303 G; 314 T; 0 other;

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alignment_scores:
  Quality: 598.50
  Ratio: 4.946
  Percent Similarity: 73.333
  Length: 1655
  Gaps: 2
  Percent Identity: 72.727
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Similarity: 73.333 Percent Identity: 72.727

Percent Similarity: 73.333 Percent Identity: 72.727

alignment_block:

Align seg 1/1 to: AAX24752 from: 1 to: 1360

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353	GTCACAGCATTTGGAAAGTAGCTGCGCCAAAGGGGAAAGTCCACGTGAATGA	402
51	ThrLeuSerLeuSerCysValAlaLysSerArgPheProAsnPheSerIl	67
403	ACGCTGAGCTTATCTGTGTGGCTGTGCAGCGGCTTCCCAACTTCACAGT	452
67	eleuThrThrPheuLysnGlySerPheIleuIleuIleuProGlnArgL	84
453	CTCTACTAGGTGGGCAATGGTCTTCATTGACACCTCCACGGCGGAC	502
84	eutPrGlnGlySerThrSerArgGlnArgLysSerThrGlnThrGlnLeu	100
503	TGTGGAGGGGAGACACGACCGGGGAAGCTGGAGACACA.....	540
101	CysLysAlaLeuValLeuGlnGlnLeuThrProAlaLeuHisSerThrAs	117
540	540
117	nPheSerCysValLeuValAsnProGlnGlnValValGlnArgHisValY	134
540	540

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134 allennalaglnleuTrpala-glyleuulrqlalrleuPropoTringl 150
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541 .....GGCTGGCTGAGGGCAACCTTGGCCCCCACCACCA 573
150 ngluAlaLeuProSerSerHisSerSerProGlnGlnGly 164
574 AGAAGCCCTCCCTCCAGCAGCAAGCATGTCCACAGCAGGAGGT 616

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seq_name: /SIDSL/gcgcdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAA11003

seq_documentation_block:

ID	standard; DNA; 495 BP.
AAAI1003	

AC AAA11003;

DT 28-JUL-2000 (first entry)

DE Mouse mature interleukin 18 binding protein coding sequence.

KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease; ss.

OS Mus musculus.

PN WO200012555-A1

PD 09-MAR-2000.

PF 18-NOV-1998; 98WO-JP05186.

PR 01-SEP-1998; 98JP-0247588.

PR 18-NOV-1998; 98JP-0327914.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Torigoe K, Tanai M, Kurimoto M,

DR WPI; 2000-237850/20.

PT Interleukin 18-binding protein with activity of regulating physiological actions of interleukin 18, useful as regulator and drug for sensitivity diseases and organ rejection and in treating diseases due to excess immune reaction

PS Claim 6; Page 57-59; 71pp; Japanese.

CC The inversion relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant
CC and in treating autoimmune diseases. This sequence represents the
CC coding sequence for the mature mouse interleukin 12 binding protein.

SQ Sequence 495 BP; 117 A; 156 C; 116 G; 106 T; 0 other;

alignment_scores:			
Quality:	515.00	Length:	158
Ratio:	3.902	Gaps:	3
Percent Similarity:	83.544	Percent Identity:	66.456

Percent Similarity: 83.544 Percent Identity: 66.456

Percent Similarity: 83.544 Percent Identity: 66.456

alignment_block:

Align seg 1/1 to: AAA11003 from: 1 to: 495

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1 ACATGTGCACCTCACAACACT.....GCCAGTGGTTTAACGTGAAGTC 44
17 rlyasProcysProSerGlnProProValAcpheProAlaAlaLysGln 34
   :-----|-----||| ||| :::: ||| :::

```

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45 AAAAGACCATCTCTCTGCTCCAGCAGTCCA...ACTAAGCAGT 91
34 yspProAlaLeuGluValThrTriProGluValGluValProLeuAsnGly 50
   |||||..... ||||| |||||..... |||||
92 ACCAGACACTGGATGTGATTTGGCCAGAAAAAGAGTCCACAGTAATGGA 141
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSer11 67
   |||||..... ||||| |||||..... |||||
142 ACCTGACCTGTCTGCTACTGCTGACGCGCTTCCCTACTTCACCAT 191
67 eleuTYTTPLeuGlyAsnGlySerPheIleGluHisLeuProGlyArgL 84
   |||||..... ||||| |||||..... |||||
192 CCTCTACTGCTGGCGAATGTTCTTCATTGACACCTTCCAGGCCGCGC 241
84 eutTPGluGlySerThrSerArgGluArgGlySerThrGlyThrGlnLeu 100
   || ||||| |||||..... ||||| |||||..... |||||
242 TGAAGGAGGGCCACACAAATCGGAGCAGACAGACACAGCAGCAGTGGCTG 291
101 CysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThrAs 117
   ::|||..... ||||| |||||..... |||||
292 CACAGGCGCTTGCTGGAGAACTGAGCCGCCACCTCAGAGAGTACCAA 341
117 nPheSerCysValLeuValAspProGluGlnValAlaGlnArgHisValY 134
   |||||..... ||||| |||||..... |||||
342 CTTCTCTCTGTTGTGTGTGATCTCGACAAAGTGGCCACATACACATCA 391
134 alleuAlaGlnLeuTrpAlaGlyLeuArgAlaThrLeuProProThrGln 150
   ::|||..... ||||| |||||..... |||||
392 TTCTGGCCGCTGCTGGGATGGGTGAAGACAGCTCCGCTTCCTTCNA 441
151 GluAlaLeuProSerSerHisSer 158
   |||::||| |||||..... |||||
442 GAAACCTC...TCTAGCCACAGC 462

seq_name: /SID1/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT:AAA11011
seq_documentation_block:
ID AAA11011 standard; DNA; 847 BP.
XX
AC AAA11011;
XX
DT 28-JUL-2000 (first entry)
XX
DE Mouse interleukin 18 binding protein complete coding sequence.
XX
KM Immunosuppressant: interleukin 18 binding protein; IL18-BP; human; mouse;
KM regulator; drug; sensitivity disease; organ rejection; organ transplant;
KM autoimmune disease; ds.
XX
OS Mus musculus.
XX
FH Location/Qualifiers
FT CDS 151..732
FT     /tag= a
FT     /product= "mouse interleukin 18 binding protein"
FT     sig_peptide 151..234
FT     mat_peptide 235..729
FT     /tag= b
FT     /tag= c
XX
PN WO200012555-A1.
PD 09-MAR-2000.
XX
PF 18-NOV-1998; 98WO-JP05186.
XX
PR 01-SEP-1998; 98JP-0247588.
PR 18-NOV-1998; 98JP-0327914.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Torioge K, Tanai M, Kurimoto M;
XX
```

```
DR WPI: 2000-237850/20.
DR P-PSDB: AAY83989.
XX
PT Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction
XX
PS Example 4; Page 67-69; 71pp; Japanese.
XX
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the coding
CC sequence for the full length mouse interleukin 12 binding protein.
XX
SQ Sequence 847 BP; 198 A; 257 C; 205 G; 187 T; 0 other;

alignment_scores:
      Quality: 515.00      Length: 158
      Ratio: 3.902      Gaps: 3
Percent Similarity: 83.544      Percent Identity: 66.456

alignment_block:
US-09-786-130-1 x AAA11011 ..

Align seg 1/1 to: AAA11011 from: 1 to: 847

1 ThrProAlaSerGlnThrThrAlaAlaThrAlaSerValArgSer17
   |||::||| |||||..... |||||::|||
235 ACATCTGACCTGCAGACACT.....GCCACGTCTTAAGTGAACCTC 278
17 rLysAspProCysProSerGlnProProValPheProAlaAlaGlyInc 34
   :|||..... ||| |||::|||
279 AAAAGACCATGCTCTCTGCTCCAGCAGTCCA...ACTAAGCAGT 325
34 yspProAlaLeuGluValThrTriProGluValGluValProLeuAsnGly 50
   |||||..... ||||| |||||..... |||||
326 ACCAGCACTGGATGTGATTTGGCCAGAAAAAGAGTCCACAGTAATGGA 375
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSer11 67
   |||||..... ||||| |||||..... |||||
376 ACTCTGACCTGTGCTGCTACTGCTGACGCGCTTCCCTACTTCACCAT 425
67 eleuTYTTPLeuGlyAsnGlySerPheIleGluHisLeuProGlyArgL 84
   |||||..... ||||| |||||..... |||||
426 CTTCTACTGCTGGCGAATGTTCTTCATTGAGCACCTTCCAGGCCGCGC 475
84 eutTPGluGlySerThrSerArgGluArgGlySerThrGlyThrGlnLeu 100
   || ||||| |||||..... ||||| |||||..... |||||
476 TGAAGGAGGGCCACACAAATCGGAGCAGACAGACACAGCAGCAGTGGCTG 525
101 CysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThrAs 117
   ::|||..... ||||| |||||..... |||||
526 CACAGGCGCTTGCTGGAGAACTGAGCCGCCACCTCAGAGAGTACCAA 575
117 nPheSerCysValLeuValAspProGluGlnValAlaGlnArgHisValY 134
   |||||..... ||||| |||||..... |||||
576 CTTCTCTCTGTTGTGTGTGATCTCGACAAAGTGGCCACATACACATCA 625
134 alleuAlaGlnLeuTrpAlaGlyLeuArgAlaThrLeuProProThrGln 150
   ::|||..... ||||| |||||..... |||||
626 TTCTGGCCGCTGCTGGGATGGGTGAAGACAGCTCCGCTTCCTTCNA 675
151 GluAlaLeuProSerSerHisSer 158
   |||::||| |||||..... |||||
676 GAAACCTC...TCTAGCCACAGC 696

seq_name: /SID1/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT:AAA11008
seq_documentation_block:
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ID      AAA11008 standard; DNA; 351 BP.
XX
AC      AAA11008;
XX
DT      28-JUL-2000 (first entry)
XX
DE      Mouse IL-18 binding protein 5' RACE fragment #1.
XX
KW      Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW      regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW      autoimmune disease; rapid amplification of cDNA ends; RACE; ss.
XX
OS      Mus musculus.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..351
FT              /*tag= a
FT              /partial
FT              /note= "fragment of N-terminus of IL-18 binding protein"
XX
PN      WO200012555-A1.
XX
PD      09-MAR-2000.
XX
PF      18-NOV-1998; 98WO-JP05186.
XX
PR      01-SEP-1998; 98JP-0247588.
PR      18-NOV-1998; 98JP-0327914.
XX
PA      (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI      Torigoe K, Tanai M, Kurimoto M;
XX
DR      WPI: 2000-237850/20.
DR      P-FSDB; AAY83986.
XX
PT      Interleukin 18-binding protein with activity of regulating
PT      physiological actions of interleukin 18, useful as regulator and drug
PT      for sensitivity diseases and organ rejection and in treating diseases
PT      due to excess immune reaction
XX
PS      Example 4; Page 65; 71pp; Japanese.
XX
SS      The invention relates to novel interleukin 18 (IL-18)-binding proteins
SS      from humans or mice which act as regulators and drugs for sensitivity
SS      diseases and organ rejection and in treating diseases due to excess
SS      immune reaction, e.g. in slowing down rejection after organ transplant,
SS      and in treating autoimmune diseases. This sequence represents the initial
SS      fragment isolated by a 5' RACE (Rapid Amplification of cDNA Ends)
SS      reaction for the 5' end of the mouse interleukin 12 binding protein
SS      coding sequence.
XX
SQ      Sequence 351 BP; 82 A; 103 C; 90 G; 76 T; 0 other;

alignment_scores:
      Quality: 441.00      Length: 112
      Ratio: 4.410      Gaps: 0
Percent Similarity: 89.286      Percent Identity: 74.107

alignment_block:
US-09-786-130-1 x AAA11008  ..

Align seg 1/1 to: AAA11008 from: 1 to: 351

32  LysGInCysProAlaLeuGluValThrTrpProGluValGluValProLeu 48
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
13  AAGCAGTACCCGACGACGTGATGTGATGGCCAGAAAAAGAGTGCCACT 62
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
48  uasnlythrleuSerleuSerCysValAlaCysSerArgPheProAsp 65
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
63  GAATGAACTGTGACCTTGTCTGTACTGCGTGCAGCGCTTCCCTACT 112
```

```
65  heserlleuTrpTrpLeuGlyAsnGlySerPheIleGluHisLeuPro 81
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
113  TCACATCCTCTACTGCTGGCAATGTTCTTCATTGAGACCTTCA 162
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
82  GlyArgLeuTrpGluGlySerThrSerArgGluArgGlySerPheGlyTh 98
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
163  GCCCGGCTGAAGGAGGCGCACACAGTCGCGAGCAGACGAAACACAC 212
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
98  rGlnLeuCysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHis 115
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
213  CTGGCTGCACAGGCGCTTGTGCTGCGAAGAACGAGCCACCTTCAGAA 262
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
115  erThrasPheSerCysValLeuValAspProGluGlnValGlnArg 131
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
263  GTACCAACTTCTCTCTGTTGTTGTTGATCTGACACAGCGCCACTAR 312
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
132  HisValValLeuAlaGlnLeuTrpAlaGlyLeuArg 143
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
313  CACATCTTCTGGCCCGCCAGCTCTGGATGGCTTGAAG 348
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

seq_name: /SIDS1/gcdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAA43451
seq_documentation_block:
ID      AAA43451 standard; CDNA; 495 BP.
XX
AC      AAA43451;
XX
DT      21-AUG-2000 (first entry)
XX
DE      Mouse secreted expressed sequence tag SEQ ID NO:26.
XX
KW      Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;
KW      expressed sequence tag; EST; probe; chemotactic; proliferative;
KW      immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
KW      thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
KW      antiviral; antidiabetic; antisthmatic; vulnerrary; antiparkinsonian;
KW      antitumor; osteopathic; neuroprotective; nootropic; antipsoriatic;
KW      cerebroprotective; anticonvulsant; antidepressant; gene therapy;
KW      vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
KW      insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KW      lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW      central nervous system disorder; Alzheimer's disease; stroke;
KW      Parkinson's disease; Huntington's disease; coagulation disorder;
KW      haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
KW      tumour; infection; depression; psoriasis; ss.
XX
OS      Mus musculus.
XX
SQ      WO200021991-A1.
XX
PD      20-APR-2000.
XX
PF      15-OCT-1999; 99WO-US24206.
XX
PR      15-OCT-1998; 98US-0104436.
XX
PA      (GEMV ) GENETICS INST INC.
XX
PI      Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI      Merberg D, Treacy M, Bowman MR;
XX
DR      WPI: 2000-317938/27.
XX
PT      Isolated polynucleotides, and encoded proteins, comprising secreted
PT      expressed sequence tags (SESTs), useful for treating various disorders
PT      such as autoimmune, infectious, and central nervous system disorders -
XX
PS      Claim 1; Page 209; 803pp; English.
XX
CC      AAA43426 to AAA45925 represent specifically claimed secreted expressed
CC      sequence tags (SESTs), isolated from human, mouse, chicken and rat
CC      tissue sources. The SESTs can have a range of activities depending on
CC      the tissues they were isolated from. The activities include:
```


128 ValValGlnArgHisValValLeuAlaGlnLeuTrpAlaGlyLeuArg 143
 |||||
 1395 GTTGTCCAGCGTCACGTCTGCTCCAGCCAGCTTGCCCTGCGAGG 1348

seq_name: /STDS1/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT:AA570676

seq_documentation_block:

ID AA570676 standard; cDNA; 7103 BP.

XX AA570676;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #6480.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW Food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR P-PSDB: ABG06489.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 1; SEQ ID NO 6480; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AA564197-AA594564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 7103 BP; 1879 A; 1805 C; 2233 G; 1185 T; 1 other;

alignment_scores:

Quality: 259.50 Length: 150
 Ratio: 3.089 Gaps: 7
 Percent Similarity: 56.000 Percent Identity: 47.333

alignment_block:
 us-09-786-130-1 x AA570676/rev ..

Align seg 1/1 to reverse of: AA570676 from: 1 to: 7103

22 ProSerGlnProProValPheProAlaAlaGlyGlnCysPro..... 35
 |||||
 2115 CCAACTCAGCCTGAATTTTATATTCAAACTGTTCCACAGTCCCTGGAGCTT 2066
 36AlaLeuGluValThrTrpProGluValGluVal 46
 2065 TTGGAGCTCATGTAGTGTATAGAGACAGATGTCATCTTCGCCAG 2016
 46 alProLeuAsnGlyThrLeuSerLeuSerCysValAlaCysSerArgPh 62
 2015 TTCCAGCTCTGATCCCTCTAGCACCTTCTGTGC.....AGATA 1978
 62 eProAsnPheserIleLeuTyTrpLeuGlyAsnGlySerPhe..... 76
 1977 CCAGGCATTC.....TGG..GGAAGAGGATGTTTTCGATT 1943
 77Ile 77
 1942 TCTGCATGACACACAACTAGAAAAACAGGTGAACCTTCTGGAAACATA 1893
 78 GlnHisLeuProGlyArgLeuTrpGluLysSerThrSerArgGluArg 94
 1892 CTTTCTCTCCCTCCGC.....TCCACCCGGGAAACGTGG 1858
 94 ySerThrGlyThrGlnLeuCysLysAlaLeuValLeuGlnLeuThrP 111
 1857 GAGCACAGGTACGACGCTGTGCAAGGCTTGCTGTGAGACAGCTGACCC 1808
 1807 CTGCCCTGCACAGCACCAACTTCTCTGTGCTGTGACCTGACCCGTGAA 1758
 111 roAlaLeuHisSerThrAsnPheserCysValLeuValAspProGlu 127
 128 ValValGlnArgHisValValLeuAlaGlnLeuTrpAlaGlyLeuArg 143
 1757 GTTGTCCAGCGTCACGTCTCTGACCAGCTTGCCCTTGCGTCGAGG 1710


```

112 GTAATGTACGCGATTACTAATTTACAGTATGTCTATTTGAT 161
      ||| |||::: :: ||| ::||| ||| ||| ||| ||| |||
71 u.....GLYAsnGlySerPheIleGluHisLeuProGlyArgLeuTrg 86
      : ::||| ::||| ||| ||| ||| ||| ||| ||| |||
162 GGTAGGTAAACAACATTCATCTCCGAGAACAACATAAGCGCATATTATA 211
      : ::||| ::||| ||| ||| ||| ||| ||| ||| |||
86 luclyser.....ThSerArgGlnArgGlySerThrGlyThnGluLeu 100
      : ::||| ::||| ||| ||| ||| ||| ||| ||| |||
212 AAGAGAAAGAAATCAATAGTACTGAATAAAAAATGGCATATGATTATGTTA 261
      : ::||| ::||| ||| ||| ||| ||| ||| ||| |||
101 CysLysAlaLeuValLeuGluGlnLeuThProAlaLeuHisSerThas 117
      ||| ::||| ::||| ||| ||| ||| ||| ||| |||
262 CGTACGCAGCTTTTATATATATATATATTTACGTCAGAAATGGAGATGACAA 311
      : ::||| ::||| ||| ||| ||| ||| ||| ||| |||
117 npheserCysValLeuValAspProGluGlnValValGlnArgHisValY 134
      : ::||| ::||| ||| ||| ||| ||| ||| ||| |||
312 ACTAACATGCTGTATTATTCAGATATATACACACCATTATCAAGCATCTATAA 361
      : ::||| ::||| ||| ||| ||| ||| ||| ||| |||
134 alleuAlaGlnLeuTPalagLYLeuArgAlaThr 145
      : ::||| ::||| ||| ||| ||| ||| ||| ||| |||
362 TATTAAATTAATTTATGGAGTTGTTTAAATCTACA 396
      : ::||| ::||| ||| ||| ||| ||| ||| ||| |||

seq_name: /cgn2_6/plodata/2/Ina/6B_COMB.seq:US-09-299-268-45

seq_documentation_block:
Sequence 45, Application US/09299268
Patent No. 6217882
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Viuela, Eliadio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,268
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/901,127
FILING DATE:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UP35.1.FWCCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:

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:      LENGTH: 405 base pairs
:      TYPE: nucleic acid
:      STRANDEDNESS: double
:      TOPOLOGY: unknown
:      MOLECULE TYPE: DNA (genomic)
US-09-299-268-45

alignment_scores:
    Quality: 106.00      Length: 95
    Ratio: 1.710        Gaps: 3
Percent Similarity: 65.263      Percent Identity: 28.421

alignment_block:
US-09-786-130-1 x US-09-299-268-45  ..

Align seg 1/1  to: US-09-299-268-45  From: 1  to: 405

57 ValAlaCysSerArgPheProAsn.....PheSerIleLeuTyrrTrpLe 71
||| |||::: :::: ||| |||::: ||| ||| ||| ||| ||| ||| |||
112 GTAAGAAATGTAACGGAATACTAATCTACGATATAGTATCTTATATTTGGAT 161
71 u.....GlyAsnGlySerPheIleGlnHisLeuProGluArgLeuTrpG 86
: ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
162 GGTAGGTAAACAACATATCATCTTCGTAGACACACTAATAATGCGATCATATA 211
: ::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
86 IuGlySer.....ThrSerArgGluArgGlySerThrGlyThrGlnLeu 100
: ::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
212 AACGAAAGAAATACATATAGTACTGCAAAAAAATGACATATCTATAAGTTA 261
101 CysLysAlaLeuValLeuGlnGlnLeuThrProAlaLeuHisSerThrAs 117
: ||| |||::: ||| ||| ||| ||| ||| ||| ||| ||| |||
262 CGTACCGACCTTATATATATATATATATACGTACGAAATGGAGATGACAAA 311
117 nPheSerCysValLeuValAspProGluGlnValAlaGlnArgHisValY 134
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
312 ACTAACAATGTGTTTATTCAGATATATACACACCATATCAAGCATCTATAA 361
134 allLeuAlaGlnLeuTrpPalaGlyLeuArgAlaThr 145
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
362 TATTATAATATTATATGAGAGTTGTTTAATACCTACA 396

seq_name: /cgn2_6/ptodata/2/ina/5A_COMP.seq:US-08-307-499-1
seq_documentation_block:
: Sequence 1, Application US/08307499
: Patent No. 5651972
: GENERAL INFORMATION:
: APPLICANT: Moyer, Richard W.
: APPLICANT: Vi uela, Eladio
: APPLICANT: Gibbs, E.P.J.
: TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
: TITLE OF INVENTION: Live Vaccine Vector
: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David R. Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: Florida
: COUNTRY: U.S.A.
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/307,499
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/908,241
: FILING DATE: 1-JUL-1992

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PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/908,630
  FILING DATE: 29-JUN-1992
  CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/342,212
    FILING DATE: 21-APR-1992
    CLASSIFICATION: 435
    ATTORNEY/AGENT INFORMATION:
      NAME: Saliwanchik, David R.
      REGISTRATION NUMBER: 31,794
    REFERENCE/DOCKET NUMBER: UF35.1.FWCCI
    TELEPHONE: 904-375-8100
    TELEFAX: 904-372-5800
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 14176 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: unknown
    MOLECULE TYPE: DNA (genomic)
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 3852..4226
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 4585..4887
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 5131..5310
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 5760..5912
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 6786..7130
    NAME/KEY: CDS
    LOCATION: 10148..10513
  US-08-307-499-1

alignment_scores:
  Quality: 106.00      Length: 95
  Ratio: 1.710        Gaps: 3
  Percent Similarity: 65.263  Percent Identity: 28.421

alignment_block:
  US-09-786-130-1 x US-08-307-499-1/rev ..

Align seg 1/1 to reverse of: US-08-307-499-1 from: 1 to: 14176
57 ValAlaCysSerArgPheProAsn.....PheSerIleuTyrTrpLe 71
   ||| |||::: ::||| ::||| ||| ||| ||| ||| ||| |||
6612 GTAAGATGTAACGATATCTAATTTCTACTATAGTATCTTATATTCAT 6563
71 u.....GLYAsnGLYSerPheIleGluHisIleuProGlyArgIleuTrpG 86
   :::: |||::: |||::: |||::: |||::: |||::: |||:::
6562 GGTAGGTAACACATACATTCGAGACACTAATATAGCGATCATTTATA 6513
86 IuGLYSer.....ThSerArgIuArgGLYSerThrGlyThrGluLeu 100
   : : : : : ||| |||::: |||::: |||::: |||::: |||:::
6512 AAGAGAGAAATACATATAGTACTGAAAAAATAGCATATGTAAGTTA 6463
101 CysLysAlaLeuValLeuGluGluIleuThrProAlaLeuHisSerThrAs 117
   |||::: |||::: |||::: |||::: |||::: |||::: |||:::
6462 CGTACCGATCTTATATATATATATATACGTCAGAAATGAGATGACAAA 6413
117 nPheSerCysValLeuValAspProGluGluIleuValGlnArgHisValY 134
   : : : : : ||| |||::: |||::: |||::: |||::: |||:::
6412 ACTAACATGTGTATTCAGATATATATACACACCTATCAAGCATCTATAA 6363

```

```

134 alleuAlaGlnIleuTyrPalaGlyLeuArgAlaThr 145
   :||| ::||| |||::: |||::: |||::: |||::: |||:::
6362 TATTAAATTAATTTATGCGCTGTCTTAATAACTACCA 6328

seq_name: /cgn2_6/ptodata/2/lna/5A_COMB.seq:US-08-307-499-14

seq_documentation_block:
  Sequence 14, Application US/08307499
  Patent No. 5651972
  GENERAL INFORMATION:
    APPLICANT: Moyer, Richard W.
    APPLICANT: Vi uela, Eladio
    APPLICANT: Gibbs, E.P.J.
  TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
  NUMBER OF SEQUENCES: 60
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: David R. Saliwanchik
    STREET: 2421 N.W. 41st Street, Suite A-1
    CITY: Gainesville
    STATE: Florida
    COUNTRY: U.S.A.
    ZIP: 32606
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/307,499
    FILING DATE:
      CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/908,241
      FILING DATE: 1-JUL-1992
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/908,630
      FILING DATE: 29-JUN-1992
      CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/342,212
      FILING DATE: 21-APR-1992
      CLASSIFICATION: 435
    ATTORNEY/AGENT INFORMATION:
      NAME: Saliwanchik, David R.
      REGISTRATION NUMBER: 31,794
    REFERENCE/DOCKET NUMBER: UF35.1.FWCCI
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 904-375-8100
      TELEFAX: 904-372-5800
  INFORMATION FOR SEQ ID NO: 14:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 14176 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: unknown
    MOLECULE TYPE: DNA (genomic)
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 138..1460
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 138..1460
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 2456..2659
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 2809..3030
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 3070..3330
    FEATURE:
      NAME/KEY: CDS
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NAME/KEY: CDS
LOCATION: 4392..5894
FEATURE:
NAME/KEY: CDS
LOCATION: 6171..6398
FEATURE:
NAME/KEY: CDS
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LOCATION: 8215..8682
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NAME/KEY: CDS
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NAME/KEY: CDS
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FEATURE:
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LOCATION: 11971..12780
FEATURE:
NAME/KEY: CDS
LOCATION: 12829..13107
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LOCATION: 13149..14171
US-08-307-499-14

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alignment_scores:
Quality: 106.00      Length: 95
Ratio: 1.710        Gaps: 3
Percent Similarity: 65.263      Percent Identity: 28.421

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alignment_block:
US-09-786-130-1 x US-08-307-499-14

Align seg 1/1 to: US-08-307-499-14 from: 1 to: 14176

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7565 GTAAATGTAACGATATCTAGCTGATCTAGCTGATCTGATCTGATCTGAT 7614
71 u.....GlyAsnGlySerPheIleGluHisLeuProGlyArgLeuTrpG 86
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7615 GGTAGTAAACAACATACATTGCTGACACACTAAATAGCATCATTTAA 7664
86 IuGlySer.....ThrSerArgGluArgGlySerThrGlyThrGlnLeu 100
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7665 AAGAGAGAAATACATATCTAGCTGAAATAATGACGATGATGATAGTAA 7714
101 CysLysAlaLeuValLeuGlnLeuThrProAlaLeuHisSerThrAs 117
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7715 CGTACGATCTTATATATATATATATACGTCGAATGAGATGACAAA 7764
117 nPheSerCysValLeuValAspProGlnValValGlnArgHisValY 134
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7765 ACTACATGTGTATATCAGATATATACACACCTATCAAGGATCTATATA 7814
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seq_name: /cgn2_6/ptodata/2/lna/6B_COMB.seq:US-09-299-268-1
seq_documentation_block:
; Sequence 1, Application US/09299268
; Patent No. 6217882
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/901,127
; FILING DATE:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCI1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14176 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3852..4226
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4585..4887
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 5131..5310
; FEATURE:
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; LOCATION: 5760..5912
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6786..7130
; FEATURE:

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APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1737
FEATURE:
NAME/KEY: misc_feature
LOCATION: 342..343
OTHER INFORMATION: /note="splice junction"
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NAME/KEY: misc_feature
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LOCATION: 756..757
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OTHER INFORMATION: /note="splice junction"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1177..1178
OTHER INFORMATION: /note="splice junction"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1350..1351
OTHER INFORMATION: /note="splice junction"
US-09-173-151A-1

alignment_scores:
Quality: 96.50      Length: 126
Ratio: 1.322        Gaps: 7
Percent Similarity: 57.937  Percent Identity: 26.190

alignment_block:
US-09-786-130-1 x US-09-173-151A-1  ..

Align seg 1/1 to: US-09-173-151A-1 from: 1 to: 1737

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3 ValserGlnThrThrAlaAlaThrAlaSerValArgSerThrLysAs 19
  ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
652 GTAAGACGACACTGAAATGAAAGTTACAGCTTACTCAGACGACCAAGCC 701
19 pProCysProSerGlnProProValPheProAlaAlaLysGlnCysProA 36
  ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
702 TCCC.....AAGCATTGTTCCCATGAGAGATCAGCCAAAGCTG 739
36 lalaGluValThrTrpGluValGluValProLeuAsnGlyThrLeu 52
  :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
740 TTATAGATGTC.....CAGCTGGGTAAAGCCTCTGAAC..... 771
53 SerLeuSerCysValAlaCysSerArgPheProAsnPhSer..... 66
  :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
772 .....ATCCCTGCAGAAAGCATTTCTTGGATTCATCGAGAGATC 809
67 .....lLeuTyTrPLeuGlnGlyAsnGlySerPheIlleGlnHisLeuP 81
  :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
810 TGGGCCAATGATCTACTGAGTGAAGAGAAAGTTATTTAGACACTGG 859
81 roGlyArgLeuTrpGluGlySer.....ThrSerArgGluArgGly 94
  ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
860 CAGGTCACTAGAGAAAGTGAATAAGCTTCTCAAGACACTTGGGA 909
95 SerThrGlnGlnGlnLeuCysLysAlaLeuValLeuGlnGlnLeuThrPr 111
  :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
910 GAAAGAGAGTTGAATG.....GCACCTCATCTTTGACTGAGTTGGGA 953
111 oAlaLeuHisSerThrAsnPhSerCys 120
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954 AGCT...GACCTGGCGAATTATACCTGC 978

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seq_documentation_block:
; Sequence 3, Application US/09173151A
; Patent No. 6326472
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Debets, Johannes Eduard Maria
; APPLICANT: Antonius
; APPLICANT: Sana, Theodore R.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins: Related Reagents and Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DMAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/173_151A
; FILING DATE: 14-OCT-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/095,987

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; FILING DATE: 10-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ. ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2058
; US-09-173-151A-3

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alignment_scores:
  quality: 96.50      Length: 126
  Ratio: 1.322      Gaps: 7
  Percent Similarity: 57.937      Percent Identity: 26.190

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US-09-786-130-1 x US-09-173-151A-3 ..

Align seq 1/1 to: US-09-173-151A-3 from: 1 to: 2061

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19 pProCysProSerGlnProProValPheProAlaAlaLysGlnCysProA 36
  ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
717 TCCC.....AAGCATTGTTCCCATGAGAGATCAGCCAAAGCTG 754
36 lalaGluValThrTrpGluValGluValProLeuAsnGlyThrLeu 52
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755 TTATAGATGTC.....CAGCTGGGTAAAGCCTCTGAAC..... 786
53 SerLeuSerCysValAlaCysSerArgPheProAsnPhSer..... 66
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67 .....lLeuTyTrPLeuGlnGlyAsnGlySerPheIlleGlnHisLeuP 81
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81 roGlyArgLeuTrpGluGlySer.....ThrSerArgGluArgGly 94
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875 CAGGTCACTAGAGAAAGTGAATAAGCTTCTCAAGACACTTGGGA 924
925 GAAAGAGAGTTGAATG.....GCACCTCATCTTTGACTGAGTTGGGA 968
111 oAlaLeuHisSerThrAsnPhSerCys 120
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seq_name: /cgn2_6/ptodata/2/lna/5A_COMB.seq:US-08-145-006C-11

seq_documentation_block:
; Sequence 11, Application US/08145006C

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20  oCysProSerGlnProVal ..... 27
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537 GAGCCCGTCGGGCGCTCCGCTCATCGCTGTGCACGCGGAGGCA 586
28  ..... 30
587 TTCGTGCCCGAGGCGCTGTGCCCTGCCCGCGGAGCTCACCCGAGC 636
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31  AlAlysGlnCysPro.....AlaLeuGlnValThrTrp..ProGluVal 44
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; INFORMATION FOR SEQ ID NO: 5

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1024 .....TCCTGCTGTGCTCTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTG 1052
59 .....CysSerArgPheProAsnPheserIleLeuTyTrpLeug 72
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1053 GCTATGCTGTGCTCA...TGGCGGCTGCTGAGCTGCACATGCTGGCCG 1099
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1100 GGCCTCCAGCAGCCGCGGCGCATCGCCG.....GGCTCC 1134
89 ThrSerArgGluArgGlySerThrGlyThrGlnLeuCysAlaLeuVal 105
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1135 ACA.....AGAGCGAGC.....GCCGGTCCAGCAGGCGCTTTGGC 1169
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1170 CTTAAAGGGCGCTGCACCTCACCACATCTGCTGGCATTTTCTTCCTCTG 1219
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-201-746-5

seq_documentation_block:
: Sequence 5, Application US/09201746
: Patent No. 6268221
: GENERAL INFORMATION:
: APPLICANT: Cone, Roger D
: APPLICANT: Mountjoy, Kathleen G
: TITLE OF INVENTION: melanocyte Stimulating Hormone Receptor
: TITLE OF INVENTION: and Uses
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
: STREET: 300 South Wacker Drive
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/201.746
: FILING DATE: 01-DEC-1998
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: NO. 6268221nan, Kevin E
: REGISTRATION NUMBER: 35,303
: REFERENCE/DOCKET NUMBER: 92,154-J
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-913-0001
: TELEFAX: 312-913-0002
: TELEX:

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: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1633 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: FEATURE:
: NAME/KEY: 5'UTR
: LOCATION: 1..461
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 462..1415
: FEATURE:
: NAME/KEY: 3'UTR
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: US-09-201-746-5

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alignment_scores:
  quality: 93.50      length: 171
  ratio: 1.184      gaps: 9
  percent similarity: 46.199      percent identity: 28.070

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alignment_block:

US-09-786-130-1 x US-09-201-746-5 ..

Align seg 1/1 to: US-09-201-746-5 from: 1 to: 1633

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939 CGGGCGCCGCGAGCCCTTGGCGGCATCTGGTGGCCAGTCTGCTTCAG 988
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989 CACGCTCTTCATCGGCTACTACGACCGCGGCGGCGGCGGCGGCGGCGG 1023
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  Patent No. 6278038
  GENERAL INFORMATION:
    APPLICANT: Come, Roger D
              Chen, Wenbiao
              Low, Malcolm J
    TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
    NUMBER OF SEQUENCES: 22
    CORRESPONDENCE ADDRESSES:
      ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
      STREET: 300 South Wacker Drive
      CITY: Chicago
      STATE: Illinois
      COUNTRY: USA
      ZIP: 60606
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      OPERATING SYSTEM: IBM PC compatible
      SOFTWARE: Patent Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/097,231
      FILING DATE: 12-Jun-1998
      CLASSIFICATION: <Unknown>
    ATTORNEY/AGENT INFORMATION:
      NAME: No. 6278038nan, Kevin E
      REGISTRATION NUMBER: 35,303
      REFERENCE/DOCKET NUMBER: 96,886-C
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 312-913-0001
      TELEFAX: 312-913-0002
      TELEX: <Unknown>
    INFORMATION FOR SEQ ID NO: 5:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 1633 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: Linear
      MOLECULE TYPE: cDNA to mRNA
      FEATURE:
        NAME/KEY: 5'UTR
        LOCATION: 1..461
      FEATURE:
        NAME/KEY: CDS
        LOCATION: 462..1415
      FEATURE:
        NAME/KEY: 3'UTR
        LOCATION: 1416..1633
      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-097-231-5

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  Quality: 93.50          Length: 171
  Ratio: 1.184           Gaps: 9
  Percent Similarity: 46.199   Percent Identity: 28.070

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15 gSerThrIlyAspProcys...ProSerGlnProProValAlaPheProAla 31
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59  .....CysSerArgRheProAsnRheSerTlleuTyrTrrleug 72
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seq_name: /cgr2_6/ptodata/2/lna/5b_COMB.seq:US-09-103-840A-2

seq_documentation_block:
: Sequence 2, Application US/09103840A
: Patent NO. 6294328
: GENERAL INFORMATION:
: APPLICANT: FLEISCHMAN, Robert D.
: APPLICANT: WHITE, Owen R.
: APPLICANT: FRASER, Claire M.
: APPLICANT: VENTER, John C.
: TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
: FILE REFERENCE: 24366-20007.00
: CURRENT APPLICATION NUMBER: US/09/103,840A
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 4403765
: TYPE: DNA
: ORGANISM: Mycobacterium tuberculosis
: FEATURE:
: OTHER INFORMATION: CDC 1551
: OTHER INFORMATION: "n" bases at various positions throughout the sequence
: OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

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Quality: 87.00 Length: 176
Ratio: 1.208 Gaps: 8
Percent Similarity: 40.909 Percent Identity: 26.136

alignment_block:
US-09-786-130-1 x US-09-103-840A-2 ..

Align seg 1/1 to: US-09-103-840A-2 from: 1 to: 4403765

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26 OValPheProAlaAlaIlyGlnCysProAlaLeuGluValThrTriProG 43
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seq_name: /cgn2_6/plodata/2/lna/5A_COMB.seq:US-07-866-979-5
seq_documentation_block:
; Sequence 5, Application US/07866979
; Patent No. 5532347
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; APPLICANT: Mountjoy, Kathleen G
; TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
; TITLE OF INVENTION: and uses
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Wilcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/866,979
; FILING DATE: 19920410
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

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; NAME: No. 5532347nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1633 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 462..1415
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..461
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1416..1633
; US-07-866-979-5

alignment_scores:
Quality: 85.50 Length: 171
Ratio: 1.110 Gaps: 9
Percent Similarity: 45.029 Percent Identity: 27.485

alignment_block:
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Align seg 1/1 to: US-07-866-979-5 from: 1 to: 1633

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889 ACATTCGATCTTCTTACGACGTGCGTACCACGACATCGTGACCCGTCGG 938
15 gSerThrIlyAspProCys...ProSerGlnProProValPheProAla 31
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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989 CAGCTCTTCATCGGCTACTACGACGACGTCGGCG..... 1023
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